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OW nucleic - nucleic search, using sw model

Run on: September 30, 2004, 00:31:06 ; Search time 2252 Seconds

(without alignments)
2167,848 Million cell updates/sec

Title: US-10-023-597-23

Perfect score: 963

Sequence: 1 aatgctgcacgaactcct.....ttttagaacaagaaga 963

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	963	100.0	963 15	US-10-023-597-23
2	755.4	78.4	931 15	US-10-017-161-1301
3	755.4	78.4	931 16	US-10-292-798-1069
4	694.2	72.1	1333 15	US-10-017-161-325
5	694.2	72.1	1333 16	US-10-292-798-291
6	693	72.0	976 15	US-10-024-399-1
7	693.4	71.9	953 16	US-10-005-041A-13
8	691.6	71.8	933 9	US-08-886-055-50
9	691.6	71.8	933 10	US-09-804-291-50
10	691.6	71.8	933 13	US-10-343-650A-395
11	691.6	71.8	933 15	US-10-220-382-35
12	657.4	68.3	1336 15	US-10-017-161-749
13	657.4	68.3	1336 16	US-10-292-798-653
14	650.6	67.6	942 13	US-10-343-650A-397

15	650.6	67.6	951 16	US-10-387-629-47	Sequence 47, App1
16	649.6	67.5	936 15	US-10-220-382-36	Sequence 36, App1
17	554.8	57.6	886 15	US-10-017-161-1299	Sequence 1299, App
18	554.8	57.6	886 16	US-10-292-798-1067	Sequence 1067, App
19	470.2	48.8	943 15	US-10-023-597-57	Sequence 57, App1
20	456.8	47.4	952 15	US-10-023-597-59	Sequence 59, App1
21	452.6	47.0	953 15	US-10-023-601-89	Sequence 89, App1
22	445.6	46.3	953 15	US-10-023-597-63	Sequence 63, App1
23	443.8	46.1	487 9	US-09-747-155-366	Sequence 366, App
24	443.6	46.1	942 15	US-10-023-601-99	Sequence 99, App1
25	443	46.0	978 15	US-10-023-601-91	Sequence 91, App1
26	436.8	45.4	934 16	US-10-024-212-21	Sequence 21, App1
27	436.8	45.4	1330 15	US-10-017-161-323	Sequence 323, App
28	436.8	45.4	1330 16	US-10-292-798-289	Sequence 289, App
29	435.6	45.2	940 15	US-10-023-597-121	Sequence 121, App
30	435	45.2	930 9	US-09-886-055-22	Sequence 22, App1
31	435	45.2	930 10	US-09-804-291-22	Sequence 22, App1
32	435	45.2	930 13	US-10-343-650A-399	Sequence 399, App
33	434.4	45.1	961 15	US-10-023-597-91	Sequence 91, App1
34	429.8	44.6	934 15	US-10-023-597-125	Sequence 125, App
35	427.6	44.4	943 15	US-10-024-399-33	Sequence 33, App1
36	425.8	44.2	961 15	US-10-023-597-91	Sequence 91, App1
37	423.2	43.9	1342 15	US-10-017-161-315	Sequence 315, App
38	423.2	43.9	1342 16	US-10-292-798-281	Sequence 281, App
39	422.8	43.9	940 15	US-10-023-601-69	Sequence 69, App1
40	422	43.8	1336 15	US-10-017-161-811	Sequence 811, App
41	422	43.8	1336 16	US-10-292-798-697	Sequence 697, App
42	422	43.8	1341 17	US-10-467-252-92	Sequence 92, App
43	421.6	43.8	1342 15	US-10-017-161-321	Sequence 321, App
44	421.6	43.8	1342 16	US-10-292-798-287	Sequence 287, App
45	421.4	43.8	915 16	US-10-387-629-71	Sequence 71, App1

ALIGNMENTS

RESULT 1
US-10-023-597-23
Sequence 23, Application US/10023597
Publication No. US20030109692A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Kekuda, Ramesh
APPLICANT: Li, Li
APPLICANT: Ballinger, Robert A.
APPLICANT: Caeman, Stacie J.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Baumgartner, Jason C.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: No. US20030109692A1e1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-224AD
CURRENT APPLICATION NUMBER: US/10/023, 597
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/256, 635
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/259, 743
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/259, 327
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: 60/261, 498
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/263, 689
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/267, 464
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: 60/271, 021
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 60/275, 946
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/278, 150
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/285, 718
PRIOR FILING DATE: 2001-04-03

Remaining Prior Application data removed - See file wrapper or PALM.
 NUMBER OF SEQ ID NOS: 128
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 23
 LENGTH: 963
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-023-597-23

Query Match 100.0%; Score 963; DB 15; Length 963;
 Best Local Similarity 100.0%; Pred. No. 2,5e-289;
 Matches 963; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 421 GTTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
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QY 961 AGA 963
DB 961 AGA 963

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RESULT 2

US-10-017-161-1301
 Sequence 1301, Application US/1001761
 Publication No. US2003014368A1
 GENERAL INFORMATION:
 APPLICANT: SUMA, MAKIKO
 APPLICANT: ASAI, KIYOSHI
 APPLICANT: AKIYAMA, YUTAKA
 APPLICANT: ABURATANI, HIROYUKI
 TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
 FILE REFERENCE: 08435/0152
 CURRENT APPLICATION NUMBER: US/10/017,161
 PRIOR FILING DATE: 2002-12-18
 PRIOR APPLICATION NUMBER: JP 2001/246789
 NUMBER OF SEQ ID NOS: 2430
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1301
 LENGTH: 931
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: source
 LOCATION: (1)..(931)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (201)..(731)
 US-10-017-161-1301

Query Match 78.4%; Score 755.4; DB 15; Length 931;
 Best Local Similarity 99.9%; Pred. No. 1.5e-224;
 Matches 756; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 267 AGAATATATTTCTCTCAAGGAGTATGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 326
DB 61 AGAATATATTTCTCTCAAGGAGTATGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 326
QY 327 TTTCTGAGTCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 386
DB 121 TTTCTGAGTCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 386
QY 387 CACTGTGTACAGATACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 446
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 QY 248 ATGATTTGTTGTCAGAGAAACATTAATTTCTTCAAGGCTGATAGTCAATCTTTC 307
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 QY 308 TTTCTGTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 367
 Db 504 TTTCTGTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 563
 QY 368 TAGTGGGATCTGTAACCCATCTGTTGTAACAGATCACATGTCCTCCAGGTTGTTG 427
 Db 564 TAGTGGGATCTGTAACCCATCTGTTGTAACAGATCACATGTCCTCCAGGTTGTTG 623
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 Db 624 CTCCTTTACTGAGTGTCTACGAGATGGGGCTTTTGGGGCTGTGCTTCAACAGAAAT 683
 QY 488 ATAGTGTCTACCTTTGTTGTCAGACAACTGTCATCACTACATGTCATGTTATGTT 547
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 QY 548 CCCCTTTGAGCTCTCTGCAACGCTTTTCAATTAATGTTCTGTTATGTT 607
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 QY 608 GTGACGTTGAGTGGGGTGGGCTTTGCTGCTTTTATCTGTTATGTTATCTT 667
 Db 804 GTGACGTTGAGTGGGGTGGGCTTTGCTGCTTTTATCTGTTATGTTATCTT 863
 QY 668 TCCAGCATCTCCGCTGATGTTGCTGAGGCAAGCTTAAAGCTTCAGTAGCTGAGC 727
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 QY 728 TCCAGCATCTCCGCTGATGTTGCTGAGGCAAGCTTAAAGCTTCAGTAGCTGAGC 787
 Db 924 TCCAGCATCTCCGCTGATGTTGCTGAGGCAAGCTTAAAGCTTCAGTAGCTGAGC 983
 QY 788 CTTTCAATTTTACCCCTGAGCAAGGGAAGTGTCTCCCTGTTCTATACACGTGAGT 847
 Db 984 CTTTCAATTTTACCCCTGAGCAAGGGAAGTGTCTCCCTGTTCTATACACATATGTC 1043
 QY 848 CCCATGTTTAAACCATTAATCTTACAGCTGAGCAATAGATGTCAACTGCTGAG 907
 Db 1044 CCCATGTTTAAACCATTAATCTTACAGCTGAGCAATAGATGTCAAAGTGTGCTGAG 1103
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RESULT 5 US-10-292-798-291

; Sequence 291, Application US/10292798
 ; Publication No. US20030235833A1

; GENERAL INFORMATION:

; APPLICANT: SUMA, MAKIHO
 ; APPLICANT: ASAI, KIYOSHI
 ; APPLICANT: AKIYAMA, YUTAKA
 ; APPLICANT: ASURAYANI, HIROYUKI
 ; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS

; FILE REFERENCE: 084335/166
 ; CURRENT APPLICATION NUMBER: US/10/292,798
 ; CURRENT FILING DATE: 2002-11-13
 ; PRIOR APPLICATION NUMBER: 10/017,161
 ; PRIOR FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: JP 2001-246789
 ; PRIOR FILING DATE: 2001-06-18
 ; NUMBER OF SEQ. ID NOS: 2070
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 ; SEQ ID NO 291
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 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; LOCATION: source
 ; FEATURE: (1)..(1333)
 ; LOCATION: (1)..(1333)
 ; NAME/KEY: CDS
 ; LOCATION: (201)..(1133)
 ; US-10-292-798-291

Query Match 72.1%; Score 694.2; DB 16; Length 1333;
 Best Local Similarity 83.7%; Pred. No. 2.4e-205;
 Matches 786; Conservative 0; Mismatches 153; Indels 0; Gaps 0.

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 QY 68 CTCACAGTCCCGCTCTCTCTGTGACAGATTATCTCGAAGGCTTAACCCACGACGCCGGA 127
 Db 264 CTCGAGATCCCGCTCTCTCTGTGACAGATTATCTCGAAGGCTTAACCCACGACGCCGGA 323
 QY 128 CTCGAGTCTGATATCTGATAGGCTCACTCTGCTGCAATCTCCCATGTAATCTTTC 187
 Db 324 CTCGAGTCTGATATCTGATAGGCTCACTCTGCTGCAATCTCCCATGTAATCTTTC 383
 QY 188 CCCCTCAACTGCTCCCTCGATGATTTAGTTCTGACAGCATATCTCCCAATGCTG 247
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 QY 428 CTCCTTTACTGAGTGTCTACGAGATGGGGCTTTTGGGGCTGTGCTTCAACAGAAAT 487
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 Db 744 CTTCTGTTGAGCTCTCTGCAACGCTTTTCAATTAATGTTCTGTTATGTTATCTT 803
 QY 608 GTGACGTTGAGTGGGGTGGGCTTTGCTGCTTTTATCTGTTATGTTATCTT 667
 Db 804 GTGACGTTGAGTGGGGTGGGCTTTGCTGCTTTTATCTGTTATGTTATCTT 863
 QY 668 TCCAGCATCTCCGCTGATGTTGCTGAGGCAAGCTTAAAGCTTCAGTAGCTGAGC 727
 Db 864 TCCAGCATCTCCGCTGATGTTGCTGAGGCAAGCTTAAAGCTTCAGTAGCTGAGC 923

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Db	184	CTTTTAACTCTTTTATATGATTTCTGTTCTCCACATCACTACTCCAAAATGCG	243
QY	248	ATGAGTTTGTCTCAAGAGAAACATTTTCTTCAACGGGTGATAGTCAATTTTC	307
Db	244	ATGAGTTTGTCTCAAGAGAAACATTTTCTTCAACGGGTGATAGTCAATGCTTTC	303
QY	308	TTCCTCTGTTCTTTGCTCTTTTCGATCCCTTCATCTCTGGGCAATGGTGAAGACGAC	367

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 Qy 368 TAGGTGGCATCTGTAAACCACTGTGTATACAGATCAACATGTCTCCAGAGTGTG 427
 Db 364 TAGGTGGCATCTGTAAACCACTGTGTATACAGATCAACATGTCTCCAGAGTGTG 423
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 Qy 488 ATAGTGTTCACCTTTTGTGACAGACACTGTGTACATCAATGTGTGATCTT 547
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 Db 544 CTCTCTTGTAGCTCTCTGTGACAGGCTTATCAATTAATGTGTGTGTGTGTG 603
 Qy 608 GTGACCGTGTGATGTGGGGTGGCCATGTGTGCGTTTATCTCTATAGGTTTATCTT 667
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 Db 784 CTTTCCATCTTCCCTGTGACAGGAGGAGTGTCTCTCTGTGTGTATACACTGTG 843
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 Db 904 AGAAGCTTTGCGAGAAAAATCTTTCTTAA 933

RESULT 9
 US-09-804-291-50
 ; Sequence 50, Application us/09804291
 ; Publication No. US20030088059A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZOZULA, SERGEY
 ; TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
 ; FILE REFERENCE: P 0278005
 ; CURRENT APPLICATION NUMBER: US/09/804,291
 ; CURRENT FILING DATE: 2001-03-13
 ; PRIOR APPLICATION NUMBER: 60/188,914
 ; PRIOR FILING DATE: 2000-03-13
 ; PRIOR APPLICATION NUMBER: 60/192,033
 ; PRIOR FILING DATE: 2000-03-24
 ; PRIOR APPLICATION NUMBER: 60/198,474
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/199,335
 ; PRIOR FILING DATE: 2000-04-24
 ; PRIOR APPLICATION NUMBER: 60/207,702
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/213,849
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: 60/226,534
 ; PRIOR FILING DATE: 2000-08-16
 ; PRIOR APPLICATION NUMBER: 60/230,732
 ; PRIOR FILING DATE: 2000-09-07
 ; PRIOR APPLICATION NUMBER: 60/266,862
 ; PRIOR FILING DATE: 2001-02-07
 ; NUMBER OF SEQ ID NOS: 529
 ; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 50
 ; LENGTH: 933
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-804-291-50
 Query Match 71.8%; Score 691.6; DB 10; Length 933;
 Best Local Similarity 84.0%; Pred. No. 1.2e-204;
 Matches 781; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

Qy 8 GCCGAGAACTCTCTCTCCGTGACAGAGTTTATCTTGTGACAGGCTTATTCACCAACCGGGA 67
 Db 4 GCAGCCAAAACCTTCTGTGACAGAGTTTATCTTGTGAGGCTTAAACCAACGCGGGA 63
 Qy 68 CTCAGAGTCCCGCTTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 127
 Db 64 CTCAGAGTCCCGCTTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 123
 Qy 128 CTGGGCTGTATTAATCTGTATAGGAGCTCAACTCTGCGCTGATATCCCATGTACTTTTTC 187
 Db 124 CTGGGCTGTATTAATCTGTATAGGAGCTCAACTCTGCACTGACATCCCATGTACTTTTTC 183
 Qy 188 CCTTCAACTGTGCTCTGATAGTTTATGTTCTGTAGACATATTCGCAAAATGCTG 247
 Db 184 CTTTTAACCTCTCTTATTAATGATTTCTGTTCTCACTAATCACTCCCAAAATGCTG 243
 Qy 248 ATGAGTTTGTCTCAAGAAACATATTTCTTGTCAAGAGGTATGAGTCAATCTTCTC 307
 Db 244 ATGAGTTTGTCTCAAGAAACATATTTCTTGTCAAGAGGTATGAGTCAATCTTCTC 303
 Qy 308 TTTCTCTGTTTCTTGTCTTCTTGTGAGTCTTCTGATCTGATCTGAGGAGTGTGAGGAGCC 367
 Db 304 TTTCTCTGTTTCTTGTCTTGTGAGTCTTCTGATCTTCTGATCTGAGGAGTGTGAGGAGCC 363
 Qy 368 TAGGTGGCATCTGTAAACCACTGTGTATACAGATCAACATGTCTCCAGAGTGTG 427
 Db 364 TAGGTGGCATCTGTAAACCACTGTGTATACAGATCAACATGTCTCCAGAGTGTG 423
 Qy 428 CTCTTTTACAGGTGTCTAGGATGGGGTGTGTTGGGGCTGTGCTATCAGAAAT 487
 Db 424 CTCTTTTGTGGGTCTATGGATGGGGTGTGCTGGGGCTGAGCCACACAGGAGC 483
 Qy 488 ATAGTGTTCACCTTTTGTGACAGACACTGTGTACATCAATGTGTGATCTT 547
 Db 484 ATATGAACCTGACCTTCTGTGTGACCACTGTGTATCAATTTATGTGTGATCTT 543
 Qy 548 CCCCTTGTAGCTCTCTGTGACAGGCTTATCAATTAATGTCTGTATCTTTATGTT 607
 Db 544 CTCTCTTGTAGCTCTCTGTGACAGGCTTATCAATTAATGTGTGTGTGTGTG 603
 Qy 608 GTGACCGTGTGATGTGGGGTGGCCATGTGTGCGTTTATCTCTATAGGTTTATCTT 667
 Db 604 GTGCTGTGTAGCTGTGATGGATGCCATGTGTCACTGTCTTATTTATGCGCTATCTC 663
 Qy 668 TCCAGCATCTCCGCGTGTATGTCTGTAGAGGAGGCTTAAAGCCTTCAGTGTGAC 727
 Db 664 TCCAGCATCTTACCAACAGTGTGTACAGAGGAGGCTTAAAGCCTTTAGTGTGAT 723
 Qy 728 TCCATCAATTTGAGTGTCTCTTTCTTTGGGTGAGAGCTTTTACGTACCTCAACCC 787
 Db 724 TCCACATTAATTTAGTGTCTCTTTCTTTGGGTGTGAGTGTGTATGTCAAAACC 783
 Qy 788 CTTTCCATTTTACCCCTGTGACAGGAGGAGTGTCTCTCTGTGTGTATACACTGTG 847
 Db 784 CTTTCCATCTTCCCTGTGACAGGAGGAGTGTCTCTCTGTGTGTATACACTGTG 843
 Qy 848 CCCATGTTTAAACCATTAATCTACAGCCTGAGATTAAGATGTCAACCTTCCCTGA 907
 Db 844 CCCGTTTAAACCATTAATCTATAGTGTGAGAAACAGATGTCAAGTGTCCCTGA 903
 Qy 908 AGAAGCTTTTCCAGATTAAGTTTTCTTGA 937
 Db 904 AGAAGCTTTGCGAGAAAAATCTTTCTTAA 933

RESULT 10
 US-10-343-650A-395
 ; Sequence 395, Application US/10343650A
 ; Publication No. US20040067499A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HAGA, TATSUYA
 ; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
 ; FILE REFERENCE: 31671-186347
 ; CURRENT APPLICATION NUMBER: US/10/343,650A
 ; PRIORITY FILING DATE: 2003-07-21
 ; PRIORITY FILING DATE: 2000-08-04
 ; PRIORITY FILING DATE: 2001-02-13
 ; NUMBER OF SEQ ID NOS: 694
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 395
 ; LENGTH: 933
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(933)
 ; US-10-343-650A-395

Query Match 71.8%; Score 691.6; DB 13; Length 933;
 Best Local Similarity 84.0%; Pred. No. 1.2e-204;
 Matches 781; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

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QY      8 GCCGAGAACTCCTCCGTCAGAGATTATCTCGAGGCTTAATCCACAGCGGGA 67
DB      4 GCAGCCAAAACCTCTGTGACAGAGTTATCTCGAAGGTTAAACCAACAGCGGGA 63
QY      68 CTCGAGGTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 127
DB      64 CTCGAGATCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 123
QY      128 CTCGAGGTCTTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 187
DB      124 CTCGAGGTCTTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 183
QY      188 CCGTTCACTTGTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 247
DB      184 CTTTAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 243
QY      248 ATGAGTTTGTCTCAAGAAAGAAATTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 307
DB      244 ATGAGTTTGTCTCAAGAAAGAAATTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 303
QY      308 TTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 367
DB      304 TTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 363
QY      368 TAGGTGGGCACTGTAAACCACTGTGTACAGATCACCAGTCTCCCAAGTGTGTTG 427
DB      364 TAGGTGGGCACTGTAAACCACTGTGTACAGATCACCAGTCTCCCAAGTGTGTTG 423
QY      428 CTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 487
DB      424 CTCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 483
QY      488 ATAGTTTCTCACTTTTGTGACAGAACTTGTCAATCACTACATGTGATGATCTT 547
DB      484 ATAGTTTCTCACTTTTGTGACAGAACTTGTCAATCACTACATGTGATGATCTT 543
QY      548 CCCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 607
DB      544 CCCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 603
QY      608 GTACAGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 667

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DB      604 GTGGCTGTGACGTTGAATGCCANTGTCACTCTCTTATTTTATGCCCCATCTC 663
QY      668 TCAGCATTCCTCCGGTAGTTCGTGAGGGGCAAGGCTTAAGCTTCAGAGGTGAGC 727
DB      664 TCAGCATTCCTCCGGTAGTTCGTGAGGGGCAAGGCTTCAGAGGTTCAGAGGTGAGC 723
QY      728 TCTTACATTAATGAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 787
DB      724 TCTTACATTAATGAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 783
QY      788 CTTTCATTTTACCCCTGAGCAGGAGGAAAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 847
DB      784 CTTTCATTTTACCCCTGAGCAGGAGGAAAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 843
QY      848 CCGATGTTTAAACCACTTAATCTCAACGCTGAGAAATAGATGCAACTTCCCTGAG 907
DB      844 CCGATGTTTAAACCACTTAATCTCAACGCTGAGAAATAGATGCAACTTCCCTGAG 903
QY      908 AGACCTTTCCAGATTAAGCTTTCTCTGA 937
DB      904 AGACCTTTCCAGATTAAGCTTTCTCTGA 933

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RESULT 11
 US-10-220-382-35
 ; Sequence 35, Application US/10220382
 ; Publication No. US2003011911A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.
 ; APPLICANT: LAU, Preethi
 ; APPLICANT: TANG, Y. Tom
 ; APPLICANT: PATTERSON, Chandra
 ; APPLICANT: YAO, Monique G.
 ; APPLICANT: SHIH, Leo L.
 ; APPLICANT: TRIBOULEY, Catherine
 ; APPLICANT: LU, Dyrung Aina M.
 ; APPLICANT: YUE, Henry
 ; APPLICANT: KEAN, Farrah A.
 ; APPLICANT: POLICKY, Jennifer L.
 ; APPLICANT: AU-YOUNG, Janice
 ; APPLICANT: YANG, Junming
 ; APPLICANT: HARLAND, Lee
 ; APPLICANT: WALSH, Roderick T.
 ; APPLICANT: LO, Terence P.
 ; APPLICANT: BOROMSKI, Mark L.
 ; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
 ; FILE REFERENCE: PI-004 PCT
 ; CURRENT APPLICATION NUMBER: US/10/220,382
 ; PRIORITY FILING DATE: 2001-03-01
 ; PRIORITY FILING DATE: 60/186,854; 60/188,384; 60/190,453; 60/190,730
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 35
 ; LENGTH: 933
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: incyte ID No. US2003011911A1 7472439CBI
 ; US-10-220-382-35

Query Match 71.8%; Score 691.6; DB 15; Length 933;
 Best Local Similarity 84.0%; Pred. No. 1.2e-204;
 Matches 781; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

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QY      8 GCCGAGAACTCCTCCGTCAGAGTTTATCTCTCGAGGCTTAATCCACAGCGGGA 67
DB      4 GCAGCCAAAACCTCTGTGACAGAGTTATCTCGAAGGTTAAACCAACAGCGGGA 63
QY      68 CTCGAGGTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 127
DB      64 CTCGAGATCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 123

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Oy	128	CTGGGCGCTGATTCCTGATAGGAGCTCAACTGCGCTGCAATATGCCCATCTGATCTTTTC	127
Oy	127	CTGGGCGCTGATTCCTGATAGGAGCTCAACTGCGCTGCAATATGCCCATCTGATCTTTTC	126
Db	124	CTGGGCTTGATTAACCTGATAGGAGCTGAACTCTACCTGACACATCCCAATGATCTTTC	123
Oy	188	CCCTTCAACTGTGCCGTGAAATTTTAGTTTCTCTACAGCAATCATATCCCAATATGCTG	247
Db	184	CTTTTAAACCTCTCTTAATATAGATTTCTGTTTCTTCACATCAATCATCCCAAAATGCTG	243
Oy	248	ATGAGTTTGTCTCAAGGAAGAAACATATATTTCTTCAAGGAGTGATATAGTCAGTTCTTC	307
Db	244	ATGAGTTTGTCTCAAGGAAGAAACATATTTCTTCTCAAGGAGTGATATAGTCAGTTCTTC	303
Oy	308	TTCTTGTGTTTCTTTTCTTTTGTGAGTCTTCATCTGTGTGGGAGATGTGAGAACCGC	367
Db	304	TTCTTGTGCTTTCTTTGTCTGTCTGTAGTCCCTTCATCTGTCAAGGATGGCCTATAGACCGC	363
Oy	368	TACGTGGGCAATCTGTAAACCACTGTGTATACAGATCACATGTCTCCCAAGTGTGTTG	427
Db	364	TAGTGGCCATCTGTAAACCACTGTGTATACAGTACACATGTCTGTGCAAGTGTGTTG	423
Oy	428	CTCTCTTTACTGGGTGTCTACGGGATGGGGGTTTTTGTGGGCTGTGCTCATACGAAAT	487
Db	424	CTCTCTTTGTGGGTGCTTATGGGATGGGGGTTTTGTGGGGCTATAGGCCACACGGAAGC	483
Oy	488	ATATGTGTTTCTACCTTTTGTGAGACACACTGTGCATACATCAATGTGAGATCTT	547
Db	484	ATATATGACCTGACCTTCTGTGTGACAACTGTGCATCATTTCAATGTGACATCTT	543
Oy	548	CCCCCTTTGAGCTCTCTCTGCAACGAGCTCTTAACATAAATGTCTGTGATCTTATTTGTT	607
Db	544	CCCTCTCTTGAAGCTCTCTCTGCAACAGCTCTTACAGAAATGAGCTGTGGTCTTATATTTG	603
Oy	608	GTAACGTTGGCAATTTGGGGGAGCCATGTGTGACGTTTTTATCTCTATATGTTTATCTT	667
Db	604	GTCGCTGTAGCTTTGGAAATGCCCATGTGCATGTCTTATTTCTATAGCCCTCATCTTC	663
Oy	668	TTCAGCACTTCTCGGCTTAGTTGTGTGTGAGGACAGGCTTAAAGCCTTCAGTACTGCAAC	727
Db	664	TTCAGCACTTCTACACAACAGTTCTACAGAAAGCAGGCTTCAAGCCTTATAGTACTTGAAT	723
Oy	728	TTCACATTAATTCAGATTTCTCTTTCTTGTGGGTGAGAGCTTTATGATCTCAAAACC	787
Db	724	TCCACATATATGTAGTTTCTCTTTCTTTGATTTGTGAGCTTTCAATGATCTCAAAACC	783
Oy	788	CTTTCCATTTTACCCCTGGAACAGGGGAAATGTCTCCCTGTTCTATACCATGTGTGTG	847
Db	784	CTTTCCATCTGTGCCCTCTGAGCAAGGAAATGTCTCCCTGTTCTATACCATATATGTC	843
Oy	848	CCCATGTTTAACCATTAATCTACAGCCTGAGAGAAATAGATGTCAAACTTGCCCTGAG	907
Db	844	CCCGTGTTAACCATTAATCTATAGCTTGAGAGAAACAGATGTCAAAAGTTCGCCCTGAGG	903
Oy	908	AGAACTTTTTCAGAAATAGACTTTTCTTGA 937	
Db	904	AGAACTTTGGCAGAAAAATCTTTTCTTGA 933	

RESULT 12
US-10-017-161-749
; Sequence 749, Application US/1001761
; Publication No. US2003014368A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKITO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 08435/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18

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? NUMBER OF SEQ ID NOS: 2430
? SOFTWARE: PatentView 2.1.1
? SEQ ID NO: 749
? LENGTH: 1336
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? TYPE: DNA
? ORGANISM: Homo sapiens
?
? FEATURE:
?
? NAME/KEY: source
?
? LOCATION: (1)..(1336)
?
? FEATURE:
?
? NAME/KEY: CDS
?
? LOCATION: (201)..(1136)
?
? OS:10-017-161-749

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Query Match	68.3%	Score 657.4;	DB 15;	Length 1336;
Best Local Similarity	80.2%;	Pred. No. 7.4e-194;		
Matches 772;	Conservative 0;	Mismatches 191;	Indels 0;	Gaps 0;

Qy	1	AATGCGTCCGAGAACTCTCTCCGCGAGAGGTTATCTCGAGGCTTATCTCAACA	60
Ds	200	AATGCGTCTGAGATTCTCTCTCGAGACAGTTTATCTCGAGGCTTATCTCAACA	259
Qy	61	GCGGAGCTCCAGGTCCCGGCTTTCCTCTGTCTAGGTTCTACGCGGACGGNGT	120
Ds	260	ACGGGAGTCCAGATCCCGGCTTCTCTCGTTTACGCTTCTACGAGTCACTGTGT	319
Qy	121	GGGGAACCTGGGCTTGATATCGATGAGGCTCACTCGCGCGACATATCCCATTA	180
Ds	320	GGGGAACCTGGGCTTGATATCGATGAGGCTCACTCACTTGCACACCCCTATGTA	379
Qy	181	CTTTTCCCTTCAACTGTCCCTCGTAGATTTTATGTTCTGTACGACCATCATTTCCAA	240
Ds	380	CTTTTCCCTTCAACTGTCTCTCATAGATTTCTGCTTTCAGAGTTATATCATCCCAA	439
Qy	241	AATGCGATGATTTGTCTCAAGAGAAACATTATTTCTTCAAGGCTGATATAGCA	300
Ds	440	AATGCGATGATTTGTCTTAAAGAAAGAACATCTCTTACGAGGCTGATATAGCA	499
Qy	301	GTTCTTCTTCTGTCTGTCTTGTCTTTTCTGAGTCTCTTCACTGTGCGCGATGNGGA	360
Ds	500	GCTCTTCTTCTTCTTCTTGTGTCTGTAGTCTTCACTCGTACGATATGACCTTA	559
Qy	361	GGACGCGTACGGGGCATCTGTACCCACAGTTGTACACAGATCAACATCTCCCCAGGT	420
Ds	560	TGACGCGTATGGGCACTGTAAACCACTGTTGTACATGTCACATGTCCTCCCAAGT	619
Qy	421	GTTGTTGCTCTTTTACTGGGNGTCTACGGGATGGGAGTTTGTGGGGCTGTGCTCATAC	480
Ds	620	GTTGTTTCTCTTTTGTGGGNGTCTATGAGGATGGGAGTTGCTGGGGCCATGCGCCACAC	679
Qy	481	AGGAATATAGGTTTCTCACTTTGTGAGAACACTGTTCATATCACTATCATGTGGA	540
Ds	680	AGGATGCAATGAGGTGTGACCTTCTGTGCCAATTAACCTTGTCAACATCAATGATGGA	739
Qy	541	CATCTTCCCTCTTGAAGCTTCTCGCAACGGCTCTTACATPAATGTCGTGTCATCTT	600
Ds	740	CATCTTCCCTCTTGAAGTGTGCTTCAACACACCTATGTGAATGAGCTGTATAGTTT	799
Qy	601	TATGTTGTGACCGTGTGCAATTGGAGGACCATTGTGTGCGGTTTTATCTATAGTTT	660
Ds	800	TGTTGTGTGGGCAATGATATGTGTGTGCCCAAGTCAACATCTTATTTCTATGCTCT	859
Qy	661	TATTTCTTCAGCAATTCGCGGTTAGTTGTGCTGTGAGGCGAAGTCTAAGCCTTCAGTGA	720
Ds	860	CATTTCTTCAGCAATCTTCCACATGTATTCACGAGGCGAGCTCCAAAGCCTTCAAGCAC	919
Qy	721	CTGACAGCTCTCAATATGAGTTTCTCTTTCTTTGGGTCAGGAGCTTATACATCT	780
Ds	920	CTGACAGCTCTCAATATGAGTTTCTCTCTTCTTTGGGTCAGGAGCATTCATATGACT	979
Qy	781	CAAAACCCCTTCATTTTAAACCTGTGACACAGGAGAAAGTGTCTCTCTGTATACAC	840
Ds	980	CAAAACCCCTTCTCTTTAGCTATGAAACAGGAGCAAGGTCTCTTCCCTATTTATACAC	1039

QY 841 TGTGTGTCCTCATGTTTAAACCATTAATCTACACCTGAGGAAATAGGATGTCAAACTTGC 900
 DB 1040 TGTGTGTCCTCATGTTTAAACCATTAATCTACACCTGAGGAAATAGGATGTCAAACTTGC 1099
 QY 901 CCTGAAGAGAACTTTTCCAGAAATAGCTTTCTGTAAAAAATTTTAAAGACAGAAAG 960
 DB 1100 TCTAAAGAAATCTTGAACAAATAGCATTTCTCTAGAAAAAGGGAATGCTCAGAAAG 1159
 QY 961 AGA 963
 DB 1160 AAA 1162
 RESULT 13
 US-10-292-798-653
 ; Sequence 653, Application US/10292798
 ; Publication No. US20030235833A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUMA, MAKIKO
 ; APPLICANT: ASAI, KIYOSHI
 ; APPLICANT: AKIYAMA, YUTAKA
 ; APPLICANT: AUBURATANI, HIROYUKI
 ; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
 ; FILE REFERENCE: 084335/166
 ; CURRENT APPLICATION NUMBER: US/10/292,798
 ; CURRENT FILING DATE: 2002-11-13
 ; PRIOR APPLICATION NUMBER: 10/017,161
 ; PRIOR FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: JP 2001-246789
 ; PRIOR FILING DATE: 2001-06-18
 ; NUMBER OF SEQ ID NOS: 2070
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 653
 ; LENGTH: 1336
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; LOCATION: source
 ; FEATURE: (1)..(1336)
 ; LOCATION: (1)..(1336)
 ; NAME/KEY: CDS
 ; LOCATION: (201)..(1136)
 US-10-292-798-653
 Query Match 68.3%; Score 657.4; DB 16; Length 1336;
 Best Local Similarity 80.2%; Pred. No. 7.4e-194;
 Matches 772; Conservative 0; Mismatches 191; Indels 0; Gaps 0;
 QY 1 AATGCTGCCGAGAACTCTCTCTCCGTGACAGATTATCTCGCAGGCTTAACTCACC 60
 DB 200 AATGCTGCCGAGAACTCTCTCTCCGTGACAGATTATCTCGCAGGCTTAACTCACC 259
 QY 61 GCCGGAGCTCCAGAGTCCCGCTTCTTCTGTTTCTAGGTTCTACGGGCTCAGGGTGT 120
 DB 260 ACCGGAGCTCCAGATCCCGCTTCTTCTGTTTCTAGGTTCTACGGGCTCAGGGTGT 319
 QY 121 GGGGAACTGGGCTTGAATATCTGATAGGGCTCAACTCTGCGCTGCAATATCCCATGA 180
 DB 320 GGGGAACTGGGCTTGAATATCTGATAGGGCTCAACTCTGCGCTGCAATATCCCATGA 379
 QY 181 CTTTTCCTCCCTCAACTGTCCTGCTAGATTGTTTCTCTACGACCATCATTCCTCAA 240
 DB 380 CTTTTCCTCCCTCAACTGTCCTGCTAGATTGTTTCTCTACGACCATCATTCCTCAA 439
 QY 241 AATGCTGATGATTTTGTCTCAAGAGAACTATTTCTTACAGGGTGTATGATCA 300
 DB 440 AATGCTGATGATTTTGTCTCAAGAGAACTATTTCTTACAGGGTGTATGATCA 499
 QY 301 GTTCTTCTTCTTCTGTTTCTTGTCTTCTTCTGAGTCTTCACTGTGCGGAGATGTGA 360
 DB 500 GCTCTTCTTCTTCTTCTTCTTGTGTCTCTGAGTCTTCACTGTGCGGAGATGTGA 559

QY 361 GGAACCCCTACGTCGGCATCTGTAAACCATCTGTTGTACACATCAACATGTCTCCCCAGGT 420
 DB 560 TGACCCGATATGGGCATCTGTAAACCATCTGTTGTACACATCAACATGTCTCCCCAGGT 619
 QY 421 GTTGTGCTCTTCTTACTGAGGTGTCTACGAGATGGGAGTTTGTGGGCTGTGCTCATAC 480
 DB 620 GTTGTGCTCTTCTTACTGAGGTGTCTACGAGATGGGAGTTTGTGGGCTGTGCTCATAC 579
 QY 481 AGGAATATAGTGTTCACCTTTTGTGACACACCTTGTCAATCACTACATGTGTGA 540
 DB 680 AGGTGATGATGGGTGTGACCTTGTGCAATCACTTGTCAACACATCACTACATGTGTGA 739
 QY 541 CATCTTCCCTTCTTGAAGTCTCTCTGCAACGCTCTTACATAATGTCTGTCATCTT 600
 DB 740 CATCTTCCCTTCTTGAAGTGTGCTGTGCAACGACCATATGTGATAGCTTGTGATGTT 739
 QY 601 TATGTTGTGACCGTTGGCATTTGGGTGCCCATTTGTCGGTTTATCTCTTATGCTTT 660
 DB 800 TATGTTGTGACCATTTGATTTGGGTGCCCATTTGTCGGTTTATCTCTTATGCTTT 859
 QY 661 TATCTTTCACGATCTCCGAGTATGTTCTGTGAGGAGGAGTCTAAAGCTTTCAGTAG 720
 DB 860 CATCTTCTCAGCATCTTCCACATTTGATTCACAGGAGGAGTCCAAAGCTTTCAGCAC 919
 QY 721 CTGACGCTCTACATTAATTTGCACTTTCTTTCTTTTGGGTGAGGAGCTTTTACGTACT 780
 DB 920 CTGACGCTCTCACAATAATTTGCACTTTCTTTCTTTTGGGTGAGGAGCTTTTACGTACT 979
 QY 781 CAAACCCCTTCATTTTAAACCTGAGACAGAGGAGAAAGTCTCCCTGTTCTATACAC 840
 DB 980 CAAACCCCTTTCTCTTTAGTATGACACAGGAGAGTCTCCCTATTTCTATACAC 1039
 QY 841 TGTGTGTCCTCATGTTTAAACCATTAATCTACACCTGAGGAAATAGGATGTCAAACTTGC 900
 DB 1040 TGTGTGTCCTCATGTTTAAACCATTAATCTACACCTGAGGAAATAGGATGTCAAACTTGC 1099
 QY 901 CCTGAAGAGAACTTTTCCAGAAATAGCTTTCTGTAAAAAATTTTAAAGACAGAAAG 960
 DB 1100 TCTAAAGAAATCTTGAACAAATAGCATTTCTCTAGAAAAAGGGAATGCTCAGAAAG 1159
 QY 961 AGA 963
 DB 1160 AAA 1162
 RESULT 14
 US-10-343-650A-397
 ; Sequence 397, Application US/10343650A
 ; Publication No. US20040067499A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAGA, YATSUYA
 ; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
 ; FILE REFERENCE: 31671-186347
 ; CURRENT APPLICATION NUMBER: US/10/343,650A
 ; CURRENT FILING DATE: 2003-07-21
 ; PRIOR APPLICATION NUMBER: JP 2000/237818
 ; PRIOR FILING DATE: 2000-08-04
 ; PRIOR APPLICATION NUMBER: JP 2001/34434
 ; PRIOR FILING DATE: 2001-02-13
 ; NUMBER OF SEQ ID NOS: 694
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 397
 ; LENGTH: 942
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(942)
 US-10-343-650A-397
 Query Match 67.6%; Score 650.6; DB 13; Length 942;
 Best Local Similarity 80.9%; Pred. No. 7.6e-192;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 29, 2004, 20:11:39 ; Search time 472 seconds

(without alignments)
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Title: US-10-023-597-23

Perfect score: 963
Sequence: 1 aatgctcgcagagactcct.....ttttagaacaagaaagaga 963

Scoring table: IDENTITY NUC
Gapop 10'-0', Gapext 1'-0'

Searched: 3373863 seqs, 212409941 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N Geneseg 29Jan04:*

1: Geneseg1980s:*\n2: Geneseg1990s:*\n3: Geneseg2000s:*\n4: Geneseg2001as:*\n5: Geneseg2001bs:*\n6: Geneseg2002s:*\n7: Geneseg2003as:*\n8: Geneseg2003bs:*\n9: Geneseg2003cs:*\n10: Geneseg2004s:*

Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	963	100.0	963	AAf88413	Aaf88413 Human GPC
2	960.4	99.7	994	AAH31675	Aah31675 Human Olf
3	937	97.3	960	ADDD12748	Addd12748 CDNA enco
4	755.4	78.4	931	ADCC8616	Adcc8616 Human GPC
5	751	78.0	935	AAH31668	Aah31668 Human Olf
6	694.2	72.1	991	ABSS8782	Abss8782 Human G-P
7	694.2	72.1	1333	ADCC85838	Adcc85838 Human GPC
8	693	72.0	976	ABK97207	Abk97207 Human G-P
9	693	72.0	976	AAAD60328	Aaad60328 Human G-P
10	692.4	71.9	953	ABT05655	Abt05655 GPCR 4 pr
11	691.6	71.8	933	AAAS15910	Aaas15910 DNA enco
12	691.6	71.8	933	AAAS42233	Aaas42233 Human CDN
13	691.6	71.8	933	ABZ43067	Abz43067 Human DNA
14	691.6	71.8	933	ABK68455	Abk68455 Human GPC
15	691.6	71.8	933	ABK37521	Abk37521 DNA enco
16	690.2	71.7	930	AAH32421	Aah32421 Human Olf
17	690.2	71.7	930	ABSS8834	Abss8834 Human G-P
18	687.4	68.3	1336	ADCC86200	Adcc86200 Human G-P
19	685.2	68.0	1655	AAAD24449	Aaad24449 Human G-P
20	650.6	67.6	942	ABZ43068	Abz43068 Human GPC
21	650.6	67.6	951	ABK68456	Abk68456 Human DNA
22	649.6	67.5	936	AAAS15911	Aaas15911 DNA enco
23	649.6	67.5	936	ABK40195	Abk40195 Human G-P

24	647.2	67.2	933	4	AAH32246	Aah32246 Human Olf
25	556	57.7	866	9	ABZ77877	Abz77877 Human G-P
26	554.8	57.6	866	9	ADCC6614	Adcc6614 Human GPC
27	480	49.8	964	4	AAH32275	Aah32275 Human Olf
28	477.4	49.6	937	6	ABSS8757	Abss8757 Human G-P
29	477.4	49.6	937	6	ABSS8759	Abss8759 Human G-P
30	477.4	49.6	937	6	ABSS8758	Abss8758 Human G-P
31	472.6	49.1	984	4	AAH32381	Aah32381 Human Olf
32	472.6	48.5	934	6	ABSS8756	Abss8756 Human G-P
33	460.6	47.8	943	9	ADDD12782	Addd12782 CDNA enco
34	460	47.8	943	9	ADDD12784	Addd12784 CDNA enco
35	458.2	47.6	942	6	AAH88430	Aah88430 Human GPC
36	456.8	47.4	952	6	AAH88431	Aah88431 Human GPC
37	454.8	47.2	945	7	ABZ77909	Abz77909 Human G-P
38	452.6	47.0	961	6	ABQ88087	Abq88087 Human GPC
39	445.6	46.3	953	6	AAH88433	Aah88433 Human GPC
40	443.8	46.1	487	4	AAH84039	Aah84039 Mouse Olf
41	443.6	46.1	942	6	ABQ88092	Abq88092 Human GPC
42	443	46.0	978	6	ABQ88088	Abq88088 Human GPC
43	441.6	45.9	962	9	ADCC79403	Adcc79403 Human G-P
44	440.8	45.8	953	9	ADDD12788	Addd12788 CDNA enco
45	436.8	45.4	934	6	ABT04145	Abt04145 Human G-P

ALIGNMENTS

RESULT 1	AAf88413 standard; CDNA; 963 BP.
ID	AAf88413
XX	AAf88413;
AC	12-NOV-2002 (first entry)
XX	Human GPCR CDNA SEQ ID 23.
DE	Human GPCR CDNA SEQ ID 23.
XX	Human, anti-HIV; nootropic; antiaesthetic; antiarteriosclerotic; GPCR;
KW	immunopressive; immunomodulator; cytosolic; antiinflammatory; AIDS;
KW	antidiabetic; neuroprotective; anorectic; haemostatic; antibacterial;
KW	fungicide; protozoal; virucide; human G-protein coupled receptor;
KW	gene therapy; vaccine; cardiomyopathy; atherosclerosis; diabetes;
KW	cell signal processing; cancer; obesity; neurodegenerative disorder;
KW	cachexia; anorexia; Alzheimer's disease; Parkinson's disease;
KW	immune disorder; graft versus host disease; bronchial asthma;
KW	Crohn's disease; multiple sclerosis; haemophilia; infectious disease;
KW	idiopathic thrombocytopenic purpura; gene; ss.
XX	
OS	Homo sapiens.
FN	WO200250275-A2.
XX	
PD	27-JUN-2002.
XX	
PF	18-DEC-2001; 2001WO-US048958.
XX	
PR	18-DEC-2000; 2000US-0256635P.
PR	21-DEC-2000; 2000US-0257876P.
PR	04-JAN-2001; 2001US-0259743P.
PR	10-JAN-2001; 2001US-0260718P.
PR	12-JAN-2001; 2001US-0261498P.
PR	24-JAN-2001; 2001US-0263689P.
PR	08-FEB-2001; 2001US-0267464P.
PR	22-FEB-2001; 2001US-0271021P.
PR	14-MAR-2001; 2001US-0275946P.
PR	23-MAR-2001; 2001US-0278150P.
PR	18-APR-2001; 2001US-0284591P.
PR	23-APR-2001; 2001US-0285718P.
PR	19-JUN-2001; 2001US-0299327P.
PR	16-AUG-2001; 2001US-0312902P.
XX	(CURA-) CURAGEN CORP.

PI Padigaru M, Kekuda R, Li L, Ballinger RA, Casman ST, Seytek KA,
 PI Baumgartner JC, Burgess CE;
 XX WPI; 2002-657419/70.
 DR P-PSDB; AAB71174.
 XX
 XX New G-protein coupled receptor polypeptides, useful in gene therapy,
 PT particularly for treating or preventing cardiovascular, atherosclerosis,
 PT diabetes, Crohn's disease, hemophilia or cancer in humans.
 XX
 XX Claim 3; Page 90; 15SP; English.

CC This invention describes novel human G-protein coupled receptor (GPCR)
 CC polypeptides which have anti-HIV, nootropic, antiallergic, antihypertensive,
 CC antiatherosclerotic, immunosuppressive, immunomodulatory, cytoskeletal,
 CC antiinflammatory, antidiabetic, neuroprotective, anorectic, haemostatic,
 CC antibacterial, fungicide and virucide activity. The products of the
 CC invention can be used in gene therapy or for vaccines. The GPCR
 CC polypeptide, GPCR nucleic acid and antibody are useful for treating,
 CC preventing or alleviating a GPCR-associated disorder or a pathological
 CC state in a subject e.g. cardiovascular, atherosclerosis, diabetes, or a
 CC disorder related to cell signal processing and metabolic pathway
 CC modulation. The GPCR polypeptide and nucleic acid are also useful for
 CC diagnosing the presence of or predisposition to a disease associated with
 CC altered levels of GPCR, particularly cancer. These polypeptides, nucleic
 CC acids and antibodies are also useful for treating or preventing obesity,
 CC neurodegenerative disorders, AIDS, cancer-associated cachexia, anorexia,
 CC Alzheimer's disease, Parkinson's disease, immune disorders, graft versus
 CC host disease, bronchial asthma, Crohn's disease, multiple sclerosis,
 CC hemophilia, idiopathic thrombocytopenic purpura or infectious disease.
 CC They can also be used to screen for potential agonist and antagonist
 CC compounds. The polypeptides are also useful as immunogens to produce
 CC antibodies or as vaccines. Anti-GPCR antibodies can be used
 CC diagnostically to monitor protein levels in tissue as part of a clinical
 CC testing procedure such as in determining the efficacy of a given
 CC treatment regimen. The host cells are useful in producing non-human
 CC transgenic animals which are useful for studying the function and/or
 CC activity of GPCR protein and for identifying and/or evaluating
 CC modulators of GPCR protein activity. AAF8402-AAF8465 encode the human
 CC GPCR proteins represented in AAB71163-AAB71226
 CC
 XX
 XX Sequence 963 BP; 193 A; 247 C; 204 G; 319 T; 0 U; 0 Other;

Query Match 100.0%; Score 963; DB 6; Length 963;
 Best Local Similarity 100.0%; Pred. No. 1e-265;
 Matches 963; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGGCTGCGAAGAACTCTCTCTGACAGATTTCCTCGAGGCTTAATCCACA 60
 DB 1 AATGGCTGCGAAGAACTCTCTCTGACAGATTTCCTCGAGGCTTAATCCACA 60
 QY 61 GCCGGAGCTCCAGGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
 DB 61 GCCGGAGCTCCAGGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
 QY 121 GGGGAACTGGGCTTATATCTGATAGGCTCAACTGCGCTGATATCCCAATGA 180
 DB 121 GGGGAACTGGGCTTATATCTGATAGGCTCAACTGCGCTGATATCCCAATGA 180
 QY 181 GGGGAACTGGGCTTATATCTGATAGGCTCAACTGCGCTGATATCCCAATGA 240
 DB 181 GGGGAACTGGGCTTATATCTGATAGGCTCAACTGCGCTGATATCCCAATGA 240
 QY 241 AATGGCTGCGAAGAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
 DB 241 AATGGCTGCGAAGAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
 QY 301 GGTCT 360
 DB 301 GGTCT 360
 QY 361 GACCGCTAGTGGGATCTGAACCACTGTTGACACGATCAACCATGCTCCCAAGT 420
 DB 361 GACCGCTAGTGGGATCTGAACCACTGTTGACACGATCAACCATGCTCCCAAGT 420

DB 361 GACCGCTAGTGGGATCTGAACCACTGTTGACACGATCAACCATGCTCCCAAGT 420
 QY 421 GGTCT 480
 DB 421 GGTCT 480
 QY 481 AGGAAATATAGTGTCTCACTTTGTCAGACAACTGTCATGACTACATAGTGTGA 540
 DB 481 AGGAAATATAGTGTCTCACTTTGTCAGACAACTGTCATGACTACATAGTGTGA 540
 QY 541 CATCT 600
 DB 541 CATCT 600
 QY 601 TATGTTGACACCTGTCATGAGGATGCGGATGTCCTTTTATCTTATAGTTT 660
 DB 601 TATGTTGACACCTGTCATGAGGATGCGGATGTCCTTTTATCTTATAGTTT 660
 QY 661 TATGTTGACACCTGTCATGAGGATGCGGATGTCCTTTTATCTTATAGTTT 720
 DB 661 TATGTTGACACCTGTCATGAGGATGCGGATGTCCTTTTATCTTATAGTTT 720
 QY 721 CTGACGCTCTCAATATGACAGTTTCTTTTCTTTGGGTCAGAGACTTTTACGTA 780
 DB 721 CTGACGCTCTCAATATGACAGTTTCTTTTCTTTGGGTCAGAGACTTTTACGTA 780
 QY 781 CAAACCCCTTCATTTTAACTCTGACACAGGAAAGTCTCTCTCTCTCTTATAC 840
 DB 781 CAAACCCCTTCATTTTAACTCTGACACAGGAAAGTCTCTCTCTCTCTTATAC 840
 QY 841 TGTGTTGACACCTGTCATGAGGATGCGGATGTCCTTTTATCTTATAGTTT 900
 DB 841 TGTGTTGACACCTGTCATGAGGATGCGGATGTCCTTTTATCTTATAGTTT 900
 QY 901 CCTGAAGAACTTTTCAAGATTAAGCTTTTCTTGAATAATTTTGAACAGAAAG 960
 DB 901 CCTGAAGAACTTTTCAAGATTAAGCTTTTCTTGAATAATTTTGAACAGAAAG 960
 QY 961 AGA 963
 DB 961 AGA 963

RESULT 2
 AAH31675
 ID AAH31675 standard; DNA; 994 BP.
 XX
 XX AAH31675;
 XX
 XX 30-JUL-2001 (first entry)
 XX
 XX Human olfactory receptor polynucleotide, SEQ ID NO: 248.
 DE Human; olfactory receptor; OR; primary scent determination;
 KM secondary scent determination; polypeptide library; odour receptor;
 KM scent profile; scent fingerprint; scent representation; ds.
 XX Homo sapiens.
 OS
 XX WO200127158-A2.
 PN
 XX 19-APR-2001.
 PD
 XX
 XX 06-OCT-2000; 2000WO-US027582.
 PF
 XX 08-OCT-1999; 99US-0158615P.
 PR 24-FEB-2000; 2000US-0184809P.
 XX (DIGI-) DIGISCENTS.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 XX Bellenson J, Smith D, Lancel D, Glusman G, Fuchs T, Yanai I;

PI Baumgartner JC, Burgess CE;
XX WPI: 2003-801280/75.
DR P-PSDB; ADD12749.
XX
PT New isolated olfactory receptor polypeptide for treating or preventing a
PT G-Protein Coupled Receptor associated disorder e.g. cardiomyopathy or
PT atherosclerosis.
XX
PS Claim 8; SEQ ID NO 23; 70bp; English.

XX The invention describes an isolated olfactory receptor polypeptide (I).
CC (I) is used to identify an agent that binds to it by contacting (I) with
CC the agent and determining binding. The agent is a cellular receptor or a
CC downstream effector. (I) is also used to identify an agent that modulates
CC the expression or activity of (I) by contacting a cell expressing (I)
CC with the agent and determining whether the agent modulates expression or
CC activity of (I). (I), or nucleic acid encoding (I), is used to treat or
CC prevent a G-protein coupled receptor (GPCR)-associated disorder in a
CC subject, preferably a human, such as cardiomyopathy or atherosclerosis,
CC or a disorder related to cell signal processing or metabolic pathway
CC modulation. (I) is used to determine the presence or predisposition to a
CC disease associated with altered levels of (I), preferably cancer, in a
CC mammal. A nucleic acid encoding (I) is used to determine the presence or
CC predisposition to a disease associated with altered levels of the nucleic
CC acid, preferably cancer, in a mammalian subject. An antibody that binds
CC to (I) is used to treat or prevent a GPCR-associated disorder, such as
CC diabetes or a disorder related to cell signal processing and metabolic
CC pathway modulation. An antibody that specifically binds (I) is used to
CC determine the presence of amount of (I) in a sample by contacting the
CC sample with the antibody and determining the presence or amount of bound
CC antibody. This sequence encodes a novel human olfactory receptor (OR), a
CC G protein coupled receptor (GPCR).
XX
SQ Sequence 960 BP; 193 A; 247 C; 202 G; 318 T; 0 U; 0 Other;

Query Match 97.3%; Score 937; DB 9; Length 960;
Best Local Similarity 99.7%; Pred. No. 3e-258;
Matches 960; Conservative 0; Mismatches 0; Indels 3; Gaps 2;

QY 1 AATGGCTGCGGAGAACTCTCTCCGCTGACAGATTATCCCGAGGCTTAATCCACA 60
DB 1 AATGGCTGCGGAGAACTCTCTCCGCTGACAGATTATCCCGAGGCTTAATCCACA 60
QY 61 GCCGGGACTCCAGGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 GCCGGGACTCCAGGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 GGGGAACTGCGGCTTATATCTCTATAGGCTCAACTCGCCGCTATATCCCACTA 180
DB 121 GGGGAACTGCGGCTTATATCTCTATAGGCTCAACTCGCCGCTATATCCCACTA 180
QY 181 CTTTTCCTCCCTCAACT 240
DB 181 CTTTTCCTCCCTCAACT 240
QY 241 AATGGCTGCGGAGAACT 300
DB 241 AATGGCTGCGGAGAACT 300
QY 301 GTTCT 360
DB 301 GTTCT 360
QY 361 GAAACGCTGAGGAGATCTGTAACCACTGTTGACAGCATCAACAGTCTCCCAAGT 420
DB 361 GAAACGCTGAGGAGATCTGTAACCACTGTTGACAGCATCAACAGTCTCCCAAGT 420
QY 421 GTTCT 480
DB 421 GTTCT 480
QY 481 AGGAATATATGTTCTCTCACTTTTGTGCAAGAACCTTGTCAATCACTATCATGTGTA 540

DB 480 AGGAATATATGTTCTCTCACTTTTGTGCAAGAACCTTGTCAATCACTATCATGTGTA 537
QY 541 CATCT 600
DB 538 CATCT 597
QY 601 TATGTTGACCGTTGAGCATTTGGGAGTCCCATTTGGTCTTTATCTCTATGTTT 660
DB 598 TATGTTGACCGTTGAGCATTTGGGAGTCCCATTTGGTCTTTATCTCTATGTTT 657
QY 661 TATCT 720
DB 658 TATCT 717
QY 721 CTGAGCT 780
DB 718 CTGAGCT 777
QY 781 CAAACCCCT 840
DB 778 CAAACCCCT 837
QY 841 TGTGAGTCCCATGTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTGC 900
DB 838 TGTGAGTCCCATGTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTGC 897
QY 901 CCTGAAGAAACCTTTTCCAGAAATAGCTTTTCTTGAATAAATTTTGAACAGAAAG 960
DB 898 CCTGAAGAAACCTTTTCCAGAAATAGCTTTTCTTGAATAAATTTTGAACAGAAAG 957
QY 961 AGA 963
DB 958 AGA 960

RESULT 4
ADCB616
ID ADCB616 standard; DNA; 931 BP.
XX
AC ADCB616;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human GPCR gene SEQ ID NO:1069.
XX
DS ds: gene; human; GPCR;
XX
KW guanosine triphosphate-binding protein coupled receptor; gene therapy.
XX
OS Homo sapiens.
XX
PN EP1270724-A2.
XX
PD 02-JAN-2003.
XX
PF 18-JUN-2002; 2002EP-00013517.
XX
PR 18-JUN-2001; 2001JP-00246789.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
PI Suwa M, Aseai K, Akiyama Y, Aburatani H;
XX
DR WPI: 2003-315783/31.
XX
DR P-PSDB; ADCB617.
XX
PT New polynucleotide, useful for preparing a composition for treating a
PT patient in need of increased or suppressed activity or expression of the
PT guanosine triphosphate-binding protein coupled receptor.
XX
PS Claim 1; SEQ ID NO 1069; 28bp; English.

CC The invention relates to a novel polynucleotide encoding a guanosine
 CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
 CC the invention may have a use in gene therapy. The polynucleotide and
 CC polypeptide are useful for preparing a composition for treating a patient
 CC in need of increased or suppressed activity or expression of the
 CC guanosine triphosphate-binding protein coupled receptor. The
 CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
 CC invention.

XX
 SQ Sequence 931 BP; 202 A; 215 C; 180 G; 334 T; 0 U; 0 Other;

Query Match 78.4%; Score 755.4; DB 9; Length 931;
 Best Local Similarity 99.9%; Pred. No. 3,9e-206;
 Matches 756; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 207 TAGATTTAGTTCTTACAGACATCATTCCTCCAAATAAGAGAGATTGTCGAAGA 266
 DB 1 TAGATTTAGTTCTTACAGACATCATTCCTCCAAATAAGAGAGATTGTCGAAGA 60
 QY 267 AGAATATTATTTCTTACAGAGTGTATGATGATGATTTCTTCTTCTTCTTCTTCT 326
 DB 61 AGAATATTATTTCTTACAGAGTGTATGATGATGATTTCTTCTTCTTCTTCTTCT 120
 QY 327 TTTCGAGTCTTATCTGTGCGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 366
 DB 121 TTTCGAGTCTTATCTGTGCGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 QY 387 CACTGTGTACAGACATCATTCCTCCAAATAAGAGAGATTGTCGAAGA 446
 DB 181 CACTGTGTACAGACATCATTCCTCCAAATAAGAGAGATTGTCGAAGA 240
 QY 447 ACGGATGAGGAGTTTGGGAGTGTGATGATGATGATTTCTTCTTCTTCTTCTTCT 506
 DB 241 ACGGATGAGGAGTTTGGGAGTGTGATGATGATGATTTCTTCTTCTTCTTCTTCT 300
 QY 507 GTGAGACACATTTCTTACAGAGTGTATGATGATGATTTCTTCTTCTTCTTCTTCT 566
 DB 301 GTGAGACACATTTCTTACAGAGTGTATGATGATGATTTCTTCTTCTTCTTCTTCT 360
 QY 567 GCAAGGCTCTTACATTAATGCTGATGATGATGATGATTTCTTCTTCTTCTTCTTCT 626
 DB 361 GCAAGGCTCTTACATTAATGCTGATGATGATGATGATTTCTTCTTCTTCTTCTTCT 420
 QY 627 TGCCATGATGATGATGATGATGATGATGATGATTTCTTCTTCTTCTTCTTCTTCT 686
 DB 421 TGCCATGATGATGATGATGATGATGATGATGATTTCTTCTTCTTCTTCTTCTTCT 480
 QY 687 GTTCGCTGAG 746
 DB 481 GTTCGCTGAG 540
 QY 747 CTCTTTCTTGGTACAGAGCTTTTACATTCCTCCAAATAAGAGAGATTGTCGAAGA 806
 DB 541 CTCTTTCTTGGTACAGAGCTTTTACATTCCTCCAAATAAGAGAGATTGTCGAAGA 600
 QY 807 ACCAGGAG 866
 DB 601 ACCAGGAG 660
 QY 867 TCTACAGCTGAGAGATTAAGAGATGATGATGATGATTTCTTCTTCTTCTTCTTCTTCT 926
 DB 661 TCTACAGCTGAGAGATTAAGAGATGATGATGATGATTTCTTCTTCTTCTTCTTCTTCT 720
 QY 927 GCTTTCTTGAAG 963
 DB 721 GCTTTCTTGAAG 757

RESULT 5
 AAH31668
 ID AAH31668 standard; DNA; 935 BP.
 XX
 AC AAH31668;

XX 30-JUL-2001 (first entry)
 DT Human olfactory receptor polynucleotide, SEQ ID NO: 241.
 DE Human olfactory receptor; OR; primary scent determination;
 XX secondary scent determination; polypeptide library; odour receptor;
 KM scent profile; scent fingerprint; scent representation; de.
 XX
 OS Homo sapiens.
 XX
 PN WO200127158-A2.
 PN 19-APR-2001.
 PD 06-OCT-2000; 2000WO-US027582.
 PF 08-OCT-1999; 99US-0158615P.
 PR 24-FEB-2000; 2000US-0184809P.
 PA (DIGI-) DIGISCENTS.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
 DR WPI; 2001-290713/30.
 XX
 PT New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists.
 XX
 PS Claim 8; Page 273; 1857pp; English.
 CC
 CC The present sequence is one of a number of isolated polynucleotides which
 CC encode polypeptides involved in olfactory sensation. The polynucleotides
 CC can be used in screening for olfactory agonists and antagonists. The
 CC methods allow for the determination of primary scents and the
 CC identification of the odour receptors used to detect these primary
 CC scents. The methods also enable determination of secondary scents and the
 CC identification of combinations of odour receptors that are involved in
 CC detecting such secondary scents. This enables the construction of a scent
 CC representation (also called a scent fingerprint or scent profile), which
 CC may be used to re-create and edit scents. Libraries of olfactory
 CC receptors are useful for determining the interaction pattern of a
 CC composition with the receptors, and can be used for determining
 CC differences in the olfactory faculties of different individuals
 CC
 SQ Sequence 935 BP; 189 A; 238 C; 190 G; 318 T; 0 U; 0 Other;

Query Match 78.0%; Score 751; DB 4; Length 935;
 Best Local Similarity 88.9%; Pred. No. 7.2e-205;
 Matches 835; Conservative 0; Mismatches 100; Indels 4; Gaps 2;

QY 2 ATGAGCTCCGAGAACTCTCTCTCTGAGAGAGATTATCTGCAAGGCTTAATCCACAG 61
 DB 1 ATGAGCTCCGAGAACTCTCTCTCTGAGAGAGATTATCTCTGCAAGGCTTAATCCACAG 60
 QY 62 CCGGAGATCCAGAGTCCCGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 121
 DB 61 CCGGAGATCCAGAGTCCCGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 120
 QY 122 GGAAGCTGGAGTGAATATCTGATAGAGGCTCACTCGCTGATATCCCATATGAC 181
 DB 121 GGAAGCTGGAGTGAATATCTGATAGAGGCTCACTCGCTGATATCCCATATGAC 180
 QY 182 TTTTCTTCTTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
 DB 181 TTTTCTTCTTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 242 ATGCTGATGATTTGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 301
 DB 241 ATGCTGATGATTTGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 297
 QY 302 TTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 361

PR 12-JAN-2001; 2001US-026198P.
PR 24-JUN-2001; 2001US-0263689P.
PR 08-FEB-2001; 2001US-0267464P.
PR 22-FEB-2001; 2001US-0271021P.
PR 14-MAR-2001; 2001US-0275946P.
PR 23-MAR-2001; 2001US-0278150P.
PR 18-APR-2001; 2001US-0284591P.
PR 23-APR-2001; 2001US-0285718P.
PR 19-JUN-2001; 2001US-0299327P.
PR 16-AUG-2001; 2001US-0312902P.

XX
XX
PA (CURAGEN) CURAGEN CORP.
XX
XX
PI Li H, Ballinger RA, Padigaru M, Kekuda R, Colman SD, Spytek KA,
PI Casan SJ, Venne CM, Sheny SC, Guev V, Mahyankar UM, Edinger S,
PI Gerlich V, Sutcheon G, Stone DJ, Sciore P, McDougall JR, Gunther E,
PI Feyman JA, Ellerman K, Gangoli EA, Millet I;
XX
XX WPI; 2002-59789/64.
DR P-SDB; ABG76802.
XX

PT New G protein coupled receptor polypeptides and polynucleotides, useful
PT in gene therapy, particularly for treating or preventing cardiomyopathy,
PT atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer
PT in humans.

XX
XX Claim 1; Page 116; 685pp; English.

PS The invention relates to novel isolated G-protein coupled receptor (GPCR)
XX polypeptides and polynucleotides. The GPCR polypeptide, GPCR nucleic acid
CC and antibody are useful for treating, preventing or alleviating a GPCR-
CC associated disorder or a pathological state in a subject, particularly a
CC human. In particular, the disorder is cardiomyopathy, atherosclerosis,
CC diabetes, or a disorder related to cell signal processing and metabolic
CC pathway modulation. The GPCR polypeptide and nucleic acid are also useful
CC for diagnosing the presence of or predisposition to a disease associated
CC with altered levels of GPCR, particularly cancer. The GPCR nucleic acid
CC and polypeptide are especially useful in therapeutic or prophylactic
CC applications for disorders associated with aberrant GPCR expression or
CC activity. The DNA encoding the protein is useful in gene therapy for
CC treating the above conditions. Furthermore, the nucleic acids and
CC polypeptides are useful in treating adenocarcinoma, lymphoma, prostate
CC cancer, uterine cancer, immune response, neurodegenerative disorders,
CC asthma, inflammatory disorders, Crohn's disease, multiple sclerosis or
CC Albritght hereditary osteodystrophy. These are also useful in developing a
CC powerful assay system for functional analysis of various human disorders,
CC as well as in diagnostic applications. AB58747-AB59231 represent human
CC GPCR coding sequences, primers and probes of the invention
XX
XX

SQ Sequence 991 BP; 205 A; 270 C; 198 G; 318 T; 0 U; 0 Other;

Query Match 72.1%; Score 694.2; DB 6; Length 991;
Best Local Similarity 83.7%; Pred. No. 1.5e-188;
Matches 786; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 8 GCCGAGAACCTCCTCCCGGTGACGAGATTATCTTCGCAGGGTTTATCATCACCAAGCGGGA 67
Db GCACCACAAAACCTCTCTGTGAAGAAGTTATCTTCGAAAGGTTAACCAACCAAGCGCGGA 111

QY 68 CTCAGGCTCCCCT 127
Db CTGCGGATCCCCCT 171

QY 128 CTGGGCTTAATCTTGATAGGGCTCAACTCGCGCTGCATATCCCATCTAATCTTTTC 187
Db CTGGGCTTAATCTTGATAGGGCTCAACTCGCGCTGCATATCCCATCTAATCTTTTC 231

QY 188 CCCTTCAACTGCCCTCGTAGATTGTTAGTTTCTCTAGACATCATCCCAAATGCTG 247
Db CTTTTTAACCTCTTTAATAGATTTCGTTTCTTCACATCAATCATCCCAAATGCTG 291

QY 248 ATAGATTTCCTCAAGAGAAACAATTATTCCTTCAACAGGCTGATAGTCACTTCTTC 307

[illegible]

RESULT 7	
ADCG85838	
ID	ADCG85838 standard; DNA; 1333 BP.
XX	
AC	ADCG85838;
XX	
DT	01-JAN-2004 (first entry)
XX	
DE	Human GPCR gene SEQ ID NO:291.
XX	
KW	ds; gene; human; GPCR;
KW	guanosine triphosphate-binding protein coupled receptor; gene therapy
XX	
OS	Homo sapiens.
XX	
PN	EP1270724-A2.
XX	
PD	02-JAN-2003.
XX	

XX 18-JUN-2002; 2002EP-00013517.
 PF
 XX
 PR 18-JUN-2001; 2001JP-00246789.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 XX (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO
 XX

PI Suwa M, Asai K, Akiyama Y, Aburatani H;
 XX WPI, 2003-315783/31.
 DR P-PSDB; ADC85839.
 XX
 XX
 PT New polynucleotide, useful for preparing a composition for treating a
 PT patient in need of increased or suppressed activity or expression of the
 PT guanosine triphosphate-binding protein coupled receptor.
 PS
 PS Claim 1; SEQ ID NO 291, 28pp; English.
 XX
 XX
 CC The invention relates to a novel polynucleotide encoding a guanosine
 CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
 CC the invention may have a use in gene therapy. The polynucleotide and
 CC polypeptide are useful for preparing a composition for treating a patient
 CC in need of increased or suppressed activity or expression of the
 CC guanosine triphosphate-binding protein coupled receptor. The
 CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
 CC invention.
 CC
 XX
 XX
 SQ Sequence 1333 BP, 266 A, 327 C, 268 G, 442 T, 0 U, 0 Other;
 Query Match 72.1%; Score 694.2; DB 9; Length 1333;
 Best Local Similarity 83.7%; Pred. No.1,7e+188;
 Matches 786; Conservative 0; Mismatches 153; Indels 0; Gaps 0

Qy	8	GCCGGAACCTCCTCCTCCGTCACAGAGTTTATCTTCGCAAGGCTTATATCCACACAGCCGGGA	67
Db	204	GCAGGCCAAAACCTTCTCTGTGACAGAGTTTATCTTCGAAGGCTTATTAACCCACACAGCCGGGA	263
Qy	68	CTCCAGGTCGCCGCTCTTCTCTGTTTCAAGGTTTCTACGCGGTGACGGTGGTGGGAAC	127
Db	264	CTGGGATGCCCTCTCTTCTCTGTTTCTGGGTTTTCACAGGTACCGGTGCGGGGAAC	323
Qy	128	CTGGGCTGTGATAATCCTGATAGGGCTCAACTCGCTGCATATCCCATGTATCTTTTC	187
Db	324	CTGGGCTGTGATAACCTGATGGGCTGAACCTGCACCTGCACATCCCATGTATCTTTC	383
Qy	188	CCCTTCAACTTGCCCTGATGATTTTATGTTTCTACAGCACCATCTTCCAAATGCTG	247
Db	384	CTTTTAACTCTCTTATATAGATTTTGTTTCTCACTACCATCACTCCAAAATGCTG	443
Qy	248	ATGAGTTTGTCTCAAGAGAAGAACTATTTCTTCACAGGGGTGATGAGTACGTTCTG	307
Db	444	ATGAGTTTGTCTCAAGAGAAGAACTATTTCTTCACAGGGGTGATGAGTACGTTCTTC	503
Qy	308	TTCCTTGTTTCTTGTCTTTTCTAGTCCCTCATCCTGTGGCGATGATGAGAGCCG	367
Db	504	TTCCTTGCTTCTTGTGCTCTGTGATCTTCATCCTGTGACGAGATGCGATGACCGG	563
Qy	368	TACGTGGGATCTGTAAACCACTGTTGTACAGATACACATGTCCTCCAGGGTGTTG	427
Db	564	TACGTGGGATCTGTAAACCACTGTTGTACAGATACACATGTTCTCCAGGGTGTTG	623
Qy	428	CTCCTTTACTGAGGTCTACAGGATGAGGAGTTTGTGGGCTGTGCTCATACAGGAAT	487
Db	624	CTCCTTTGTGGGTGCTATAGGATGAGGAGTTTGTGGGCTGTGCTCATACAGGAAGC	683
Qy	488	ATATGTTTCTCACTTTTGTGAGACAACTGTCAATACACAAATGTGTGATCTCTT	547
Db	684	ATATAGAACTGACCTTCTGTGTGCAACCTGTCAATATTTCAATGTGTGACATCTT	743
Qy	548	CCCTCTTGAGCTCTCTGCAACCGGCTTTACATAATGTCCGTGCATCTTTATTTGT	607
Db	744	CTCTCTTGAGCTCTCTCTGCAACCGGCTTTACATAATGAGCTGGTGGCTTTATTTGTG	803
Qy	608	GTCACGCTTGACATTTGGGTGCCCATTTGTCGCGTTTATCTCTTATGGTTTATCTT	667
Db	804	GTCACGCTTGACATTTGGGATGCCCATTTGTACTGTCTTTATTTCTTATGCCCTCATCTC	863
Qy	668	TCCAGCATTCCTCGCGTTAGTTCTGCTGAGGGGAGGCTTAAAGCTTCAGTACGTGACG	727
Db	864	TCCAGCATTCACACAACAGTTTCTTACAGGAAGGAGGCTCAAAAGCTTTAGTACTTGGAGT	923

QY 728 TCCTACATAATTGACATTTCTTTCTTTGTTGGTACAGACTTTTACGTAAGTCAAAACC 787
 Db 924 TCCACATATATGATGTTCTTTCTTTGTTGGTACAGACTTTTACGTAAGTCAAAACC 983
 QY 788 CCTTCATTTTACCCCTGACAGAGGAAAGTCTCTCCCTGTTCTATACCACTGTGTC 847
 Db 984 CTTTCATCTCTGCTCCCTGACAGAGGAAAGTCTCTCCCTGTTCTATACCACTATAGTTC 1043
 QY 848 CCCATGTTTACCCATTAATCTACAGCTGAGAAATAGAGTCAAACTTGCCTGAG 907
 Db 1044 CCGGTGTTAAACCCATTAATCTATAGCTTGAAGAACAGAGTGTCAAACTTGCCTGAG 1103
 QY 908 AGAACCTTTTCCAGAAATAGCTTTTCTTGAATAAAATTT 946
 Db 1104 AGAACCTTTGAGCAAGAAATCTTTTCTTAAGAAAGATT 1142

RESULT 8
 ABK97207
 ID ABK97207 standard; cDNA; 976 BP.
 AC ABK97207;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Human G-protein coupled receptor (GPCR) GPCR gene #1.
 XX
 KW G-protein coupled receptor; receptor; GPCR; GPCR; cardiomyopathy;
 KW atherosclerosis; diabetes; cell signal processing; cancer; trauma;
 KW metabolic pathway; modulation; neuro-olfactory system; surgery;
 KW neoplastic disorder; adenocarcinoma; lymphoma; prostate cancer;
 KW uterine cancer; immune response; acquired immunodeficiency syndrome; AIDS;
 KW asthma; Crohn's disease; multiple sclerosis;
 KW Albinism hereditary osteodystrophy; gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200250117-A2.
 XX
 PD 27-JUN-2002.
 XX
 PF 18-DEC-2001; 2001WO-US049077.
 XX
 PR 18-DEC-2000; 2000US-0256635P.
 XX
 PR 21-DEC-2000; 2000US-0257876P.
 PR 04-JAN-2001; 2001US-0259743P.
 PR 10-JAN-2001; 2001US-0260718P.
 PR 12-JAN-2001; 2001US-0261498P.
 PR 24-JAN-2001; 2001US-0263689P.
 PR 08-FEB-2001; 2001US-0267464P.
 PR 22-FEB-2001; 2001US-0271021P.
 PR 14-MAR-2001; 2001US-0275946P.
 PR 23-MAR-2001; 2001US-0278150P.
 PR 18-APR-2001; 2001US-0284591P.
 PR 23-APR-2001; 2001US-0285718P.
 PR 19-JUN-2001; 2001US-0293327P.
 PR 16-AUG-2001; 2001US-0312902P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Padigam M, Kehruda R, Colman SD, Spytek KA, Ballinger RA;
 PI Verneel CM, Li L, Shenoy S, Casman SJ;
 DR WPI; 2002-528447/56.
 DR P-PSDB; ABG68134.
 XX
 XX New G-protein coupled receptor polypeptides for treating or preventing
 PT cardiomyopathy, atherosclerosis, diabetes, multiple sclerosis, acquired
 PT immunodeficiency syndrome or cancer in humans.
 XX
 XX Claim 5; Page 79; 110pp; English.

CC The present invention relates to a new G-protein coupled receptor (GPCR) CC
 CC polypeptide. The GPCR polypeptide, GPCR nucleic acid and antibody are CC
 CC useful for treating, preventing or alleviating a GPCR-associated CC
 CC disorder or a pathological state in a subject, particularly a human. In CC
 CC particular, the disorder is cardiomyopathy, atherosclerosis, diabetes, or CC
 CC a disorder related to cell signal processing and metabolic pathway CC
 CC modulation. The GPCR polypeptide and nucleic acid are also useful for CC
 CC diagnosing the presence of or predisposition to a disease associated with CC
 CC altered levels of GPCR, particularly cancer. The GPCR nucleic acid and CC
 CC polypeptide are especially useful in therapeutic or prophylactic CC
 CC applications for disorders of the neuro-olfactory system, e.g., those CC
 CC induced by trauma, surgery and/or neoplastic disorders. The DNA encoding CC
 CC the protein is useful in gene therapy for treating the above conditions. CC
 CC Furthermore, the nucleic acids and polypeptides are useful in treating CC
 CC adenocarcinoma, lymphoma, prostate cancer, uterine cancer, immune CC
 CC response, acquired immunodeficiency syndrome (AIDS), asthma, Crohn's CC
 CC disease, multiple sclerosis or Albinism hereditary osteodystrophy. These CC
 CC are also useful in developing powerful assay system for functional CC
 CC analysis of various human disorders, as well as in diagnostic CC
 CC applications. The present nucleic acid sequence represents one of a CC
 CC collection (ABK97207-ABK97226) of human GPCR genes that encode the human CC
 CC GPCR proteins (AAU68134-AAU68153) of the invention CC
 XX

Sequence 976 BP; 204 A; 259 C; 204 G; 309 T; 0 U; 0 Other;
 SQ

Query Match 72.0%; Score 693; DB 6; Length 976;
 Best Local Similarity 83.5%; Pred. No. 3.3e-188;
 Matches 786; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 1 AATGCTGCGGAGAACTCCCTCCGTCACAGATTTATCCCGAGGCTTATCCACCA 60
 Db 7 AATGCGCCAGCCCAAAATCTCTGTGACAGATTTATCCCGAGGCTTAAACCAACA 66
 QY 61 GCGGAGATCCAGATCCCGTCTTCTCTGTTTCTAGATTTCTACGGGCTCAAGGTGT 120
 Db 67 GCGGAGATCCAGATCCCGTCTTCTCTGTTTCTAGATTTCTACGGGCTCAAGGTGT 126
 QY 121 GGGGAACCTGGGCTGATATATCTGATAGGCTCACTGCTGCAATCCCATGTA 180
 Db 127 GGGGAACCTGGGCTGATATATCTGATAGGCTCACTGCTGCAATCCCATGTA 186
 QY 181 CTTTTCCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 Db 187 CTTTTCCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 246
 QY 241 AATGCTGATGATTTGTTCTCAAGAGAACATATTTCTTCAAGGCTGATGATCA 300
 Db 247 AATGCTGATGATTTGTTCTCAAGAGAACATATTTCTTCAAGGCTGATGATCA 306
 QY 301 GTTCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 Db 307 GTTCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 366
 QY 361 GACCGCTAGTGGGCTGATGTAACCACTGTTGATACAGATCAAGTCTCCCAAGT 420
 Db 367 TGACCGCTAGTGGGCTGATGTAACCACTGTTGATACAGATCAAGTCTCCCAAGT 426
 QY 421 GTGTTGCTCTTTTACGCGGTCTACAGGATGGGGGTTTGGGCTGTGCTCATAC 480
 Db 427 GTGTTGCTCTTTTACGCGGTCTACAGGATGGGGGTTTGGGCTGTGCTCATAC 486
 QY 481 AGAAATATAGTGTTCACCTTTGTGACAGAACCTTGTCAATCACTACATAGTGA 540
 Db 487 AGAAATATATGAAACCGACCTTCTGTGACAGAACCTTGTCAATCACTACATAGTGA 546
 QY 541 CATCTTCCCTTTCTGAGCTCTCTGCAACGGCTCTTAACATAAAGTCTGTGATCTT 600
 Db 547 CATCTTCCCTTTCTGAGCTCTCTGCAACGGCTCTTAACATAAAGTCTGTGATCTT 606
 QY 601 TATGTTGTGACCTTGGCATTTGGGGTGGCCATTTGTGCGGTTTATCTTATGTTT 660
 Db 607 TATGTTGTGCTTGAAGTGAATGCCATTTGATCTGCTTATTTCTTATGCTCT 666

QY 661 TATCTTTCGAGCATTCGCGCTAGTCTGCGAGGGGCTTAAGCCTTCAGTAG 720
 DB 667 CATCTCTCCGAGCATTTCTACACAGATTTCTACAGAGGAGGCTCAAGCCTTTAGTAC 726
 QY 721 CTGAGCTCTCTACATTAATGCAAGTTCTCTTTCTTTGGTGACAGAGCTTTTACGTA 780
 DB 727 TTGAGTTCCCAATTAATGATTTCTCTTTCTTTGTTGTTGTTGTTGTTGTTGTTGTT 786
 QY 781 CAACACCCCTCTCTCTTTTACCCCGAGACGAGGAGAAAGTCTCTCTCTCTCTCTCTCT 840
 DB 787 CAACACCCCT 846
 QY 841 TGTGCTGCGCATGTTTAAACCATTAATCTACAGCTTGAGGAAATAGAGATGCTCAACTTC 900
 DB 847 AATAGTCCCGTGTAAACCATTAATCTAGCTTGAGGAAATAGAGATGCTCAACTTC 906
 QY 901 CCTGAAGGAGACCTTTCCGAAATTAAGCTTTCTTGTGAAA 941
 DB 907 CCTGAGGAGACCTTTGGGCAAGAAAATCTTTCTTAAGAAA 947

RESULT 9
 AAD60328
 ID AAD60328 standard; DNA; 976 BP.
 AC AAD60328;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human G-protein coupled receptor (GPCR) GPCR DNA #1.
 XX
 KW Human: G-protein coupled receptor; GPCR; stroke; obesity; vitinucle;
 KW multiple sclerosis; Alzheimer's disease; graft-versus-host disease;
 KW endometriosis; tissue typing; gene therapy; vaccine; antibacterial;
 KW retinal disease; infection disease; bulimia; receptor; fungicide;
 KW Parkinson's disease; hypertension; acute heart failure; infection;
 KW cardiomyopathy; atherosclerosis; diabetes; detectability disorder;
 KW cancer; signal transduction pathway disorder; metabolic disorder;
 KW developmental disorder; osteoporosis; protozoicide; asthma; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 8..943
 FT /*tag= a
 FT /product= "Human GPCR protein"

US2003100491-A1.
 XX
 PD 29-MAY-2003.
 XX
 PF 18-DEC-2001; 2001US-00024399.
 XX
 PR 18-DEC-2000; 2000US-0256635P.
 PR 21-DEC-2000; 2000US-0257876P.
 PR 04-JAN-2001; 2001US-0259743P.
 PR 10-JAN-2001; 2001US-0260718P.
 PR 12-JAN-2001; 2001US-0261498P.
 PR 24-JAN-2001; 2001US-0263689P.
 PR 08-FEB-2001; 2001US-0267464P.
 PR 22-FEB-2001; 2001US-0271021P.
 PR 14-MAR-2001; 2001US-0275946P.
 PR 23-MAR-2001; 2001US-0278150P.
 PR 18-APR-2001; 2001US-0284581P.
 PR 23-APR-2001; 2001US-0285718P.
 PR 19-JUN-2001; 2001US-0293277P.
 PR 16-AUG-2001; 2001US-0312902P.
 XX
 PA (PADI/) PADIGARU M.
 PA (KERU/) KERUDA R.
 PA (COLM/) COLMAN S. D.
 PA (SPYK/) SPYTEK K. A.
 PA (BALL/) BALLINGER R. A.

PA (VERN/) VERNET C. A. M.
 PA (LILU/) LI L.
 PA (SHEN/) SHENOY S. G.
 PA (CASW/) CASMAN S. J.
 PI Padigaru M., Kekuda R., Colman SD., Spytek KA., Ballinger RA,
 PI Vernet CM, Li L., Sheno Sg., Casman SJ;
 XX
 DR MPI; 2003-755210/71.
 XX P-PSDB; AAB39659.
 PT New G-protein coupled receptor (GPCR) polypeptides and nucleic acids,
 PT useful for diagnosing, preventing or treating GPCR-associated disorders,
 PT e.g. cardiomyopathy, atherosclerosis, cancer or diabetes, and in
 PT pharmacogenomics.
 XX
 PS Claim 8; Page 32; 46pp; English.
 CC The invention relates to G-protein coupled receptor (GPCR) polypeptides
 CC (designated as GPCR) and nucleic acid sequences. GPCR polypeptides,
 CC nucleic acids and antibodies are useful in diagnosing, preventing or
 CC treating GPCR-associated disorders, such as cardiomyopathy, diabetes,
 CC atherosclerosis and cancer. These may also be used for treating or
 CC preventing other diseases like developmental disorders, taste and scent
 CC detectability disorders, signal transduction pathway disorders, retinal
 CC diseases, metabolic disorders (e.g. obesity), infectious diseases (e.g.
 CC bacterial, fungal, protozoal or viral infections), bulimia, asthma,
 CC Parkinson's disease, hypertension, acute heart failure, osteoporosis,
 CC multiple sclerosis, Alzheimer's disease, stroke, graft-versus-host
 CC disease or endometriosis. GPCR nucleic acid is used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. It is also useful in gene therapy. GPCR is useful as
 CC vaccines. The present sequence is human GPCR DNA
 XX
 SQ Sequence 976 BP; 204 A; 259 C; 204 G; 309 T; 0 U; 0 Other;
 Query Match 72.0%; Score 693; DB 9; Length 976;
 Best Local Similarity 83.5%; Pred. No. 3.3e-188;
 Matches 786; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 1 AATGGTCGCGAGACCTCTCTCGTGAAGAGGTTTACCTGCGAGGTTATCCAGCA 60
 DB 7 AATGGTCGCGAGACCTCTCTCGTGAAGAGGTTTACCTGCGAGGTTATCCAGCA 66
 QY 61 GCCGGGACTCCAGGTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
 DB 67 GCCGGGACTCCAGGTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 126
 QY 121 GGGGAACCTGGGCTGATTAATCTGATAGGCTCACTCGCTGCAATATCCCACTGA 180
 DB 127 GGGGAACCTGGGCTGATTAATCTGATAGGCTCACTCGCTGCAATATCCCACTGA 186
 QY 181 CTTTTCCTCTCACT 240
 DB 187 CTTTTCCTCTCACT 246
 QY 241 AATGCTATAGTTTGTCTCAAGGAAGAACATTAATCTCTCAAGGCTGATAGTGA 300
 DB 247 AATGCTATAGTTTGTCTCAAGGAAGAACATTAATCTCTCAAGGCTGATAGTGA 306
 QY 301 GTTCT 360
 DB 307 GTTCT 366
 QY 361 GGAGCGCTAGCGGCTCTGTAACCACTGTTGTAAGATATACATATCTCCAGGT 420
 DB 367 TGACCGCTAGCGGCTCTGTAACCACTGTTGTAAGATATACATATCTCCAGGT 426
 QY 421 GTGTTGCT 480
 DB 427 GTGTTGCT 486
 QY 481 AGGAATATATAGTTTGTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540

Db 304 TTCTTCTGCTCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 363
 Qy 368 TAGTGGGATCTGTATACCACTGTGTATACAGATCACCATGCTCCAGGTTGG 427
 Db 364 TAGTGGGATCTGTATACCACTGTGTATACAGATCACCATGCTCCAGGTTGG 423
 Qy 428 CTCTCTTCTGCTCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 487
 Db 424 CTCTCTTCTGCTCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 483
 Qy 488 ATAGTCTTCTGCTCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 547
 Db 484 ATATGATCTGATCTTCTGTGTGACCACTTGTATATCTTGTATGATGATG 543
 Qy 548 CCCCTTCTGCTCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 607
 Db 544 CCTCTCTGCTCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 603
 Qy 608 GTGACGCTGCTGCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 667
 Db 604 GTGACGCTGCTGCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 663
 Qy 668 TCCAGATCTTCTGCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 727
 Db 664 TCCAGATCTTCTGCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 723
 Qy 728 TCCATCATATGCTGCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 787
 Db 724 TCCATCATATGCTGCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 783
 Qy 788 CCTCTCTGCTCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 847
 Db 784 CCTCTCTGCTCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 843
 Qy 848 CCTCTCTGCTCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 907
 Db 844 CCTCTCTGCTCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 903
 Qy 908 AGAAGCTTTCTGCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 937
 Db 904 AGAAGCTTTCTGCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 933
 RESULT 12
 AAS42233
 ID AAS42233 standard; cDNA; 933 BP.
 AC AAS42233;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human cDNA encoding olfactory receptor AOLFPR26.
 XX
 KW Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;
 XX ss; food additive; cosmetic; fragrance; pharmaceutical additive.
 OS Homo sapiens.
 PN M0200168805-A2.
 PD 20-SEP-2001.
 XX
 PF 13-MAR-2001; 2001WO-US007771.
 XX
 PR 13-MAR-2000; 2000US-0188914P.
 PR 24-MAR-2000; 2000US-0192033P.
 PR 12-APR-2000; 2000US-0198474P.
 PR 24-APR-2000; 2000US-0199315P.
 PR 26-MAY-2000; 2000US-0207782P.
 PR 23-JUN-2000; 2000US-0213849P.
 PR 16-AUG-2000; 2000US-0226534P.
 PR 07-SEP-2000; 2000US-0230732P.
 PR 07-FEB-2001; 2001US-0268682P.

XX (SENSO-) SENOMYX INC.
 PA Zozulya S;
 PI WPI; 2001-570867/64.
 XX P-PSDB; AAU24540.
 DR
 PT Nucleic acid encoding human olfactory G protein-coupled receptors,
 PT useful for screening for compounds involved in olfactory sensation, where
 PT the compounds can be used in the food, pharmaceutical and cosmetic
 PT industries to customize odors.
 XX
 PS Claim 1; Page 94; 31pp; English.
 CC The invention relates to nucleic acids encoding human olfactory
 CC receptors, OR, (a G protein-coupled receptor, GPCR). The OR's
 CC specifically recognise molecules, odourants, that elicit specific
 CC olfactory sensation. The human olfactory receptors and polynucleotides
 CC encoding them are useful for screening a library of chemical compounds
 CC for compounds that are involved in olfactory sensation. Modulators of
 CC their activity are useful for pharmacological and genetic modulation of
 CC olfactory signalling pathways. Therefore, they can be used in the food,
 CC pharmaceutical and cosmetic industries to customize odours and
 CC fragrances. The present sequence encodes a human olfactory receptor of
 CC the invention
 CC
 SQ Sequence 933 BP; 192 A; 251 C; 188 G; 302 T; 0 U; 0 Other;
 Query Match 71.8%; Score 691.6; DB 5; Length 933;
 Best Local Similarity 84.0%; Pred. No. 8,1e-188;
 Matches 781; Conservative 0; Mismatches 149; Indels 0; Gaps 0;
 Qy 8 GCCGAACTCTCTCTCTCTGACAGATTTATCTGAGGCTTATCCACAGCCGGA 67
 Db 4 GCCGAACTCTCTCTCTCTGACAGATTTATCTGAGGCTTATCCACAGCCGGA 63
 Qy 68 CTCAGAGTCCCGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 127
 Db 64 CTCAGAGTCCCGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 123
 Qy 128 CTGGGCTGATATCTGATAGGCTCACTCTGCTGCTGCTGCTGCTGCTGCTGCT 187
 Db 124 CTGGGCTGATATCTGATAGGCTCACTCTGCTGCTGCTGCTGCTGCTGCTGCT 183
 Qy 188 CCTTCAACTCTGCT 247
 Db 184 CCTTCAACT 243
 Qy 248 ATGAGTTTGTCTCAAGGAAGATTTATCTCTCTCTCTCTCTCTCTCTCTCTCT 307
 Db 244 ATGAGTTTGTCTCAAGGAAGATTTATCTCTCTCTCTCTCTCTCTCTCTCTCT 303
 Qy 308 TTTCT 367
 Db 304 TTTCT 363
 Qy 368 TACGAGGATCTGTAAACCACTGTGTACACATCTCTCTCTCTCTCTCTCTCTCT 427
 Db 364 TACGAGGATCTGTAAACCACTGTGTACACATCTCTCTCTCTCTCTCTCTCTCT 423
 Qy 428 CTCTCTTCTGCTCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 487
 Db 424 CTCTCTTCTGCTCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 483
 Qy 488 ATAGTCTTCTGCTCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 547
 Db 484 ATATGATCTGATCTTCTGTGTGACCACTTGTATATCTTGTATGATGATG 543
 Qy 548 CCCCTTCTGCTCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 607
 Db 544 CCTCTCTGCTCTTTTGTCTGTGAGTCTTCTGACGATGCGATGACCGC 603

QY 608 GTGACCGTTGGCATTTGGGGTCCCATTTGCGCTTTTATCTTATGTTTATTCTT 667
 DB 604 GTGGCTGTGAGCTTGAGATGCCCATGTGACATCTCTTTATTTCTTATGCTTCACTC 663
 QY 668 TCCAGCATTTCTCGCGGTAGTTCTGCTGAGGCGAGCTTAAGCCTTCACTAGCTGACAG 727
 DB 664 TCCAGCATTTCTACACAGAGTTCTACAGAGGCGAGCTTCAAGCCTTCACTAGCTGACAG 723
 QY 728 TCCATCAATTAATGAGTTCTCTTTCTTTGGTGGTCAAGAGCTTTACGTTCCCAACCC 787
 DB 724 TCCACATTAATTTAGTTCTCTTTCTTTGGTGGTCAAGAGCTTTACGTTCCCAACCC 783
 QY 788 CTTTCATATTTTACCCCTGAGACGAGGAGAAAGTCTCTCTGTTCTTATACACTGTGTG 847
 DB 784 CTTTCATATCTGCGCCCTGAGACGAGGAGAAAGTCTCTCTGTTCTTATACACTATAGTC 843
 QY 848 CCGATGTTTAAACCATTAATCTACAGCGCTGAGAAATAGATGCAACTGTGCGTGAAG 907
 DB 844 CCGGTGTTAAACCATTAATCTATAGCTTGAAGAACAGAGATGCAAGTTGCGCTGAGG 903
 QY 908 AGAACCTTTTCCAGAAATAGCTTTTCTTGA 937
 DB 904 AGAAGTTGGGCGAGAAATCTTTCTTAA 933

RESULT 13
 AB243067 standard; DNA; 933 BP.
 AB243067
 AC 06-04-2003 (first entry)
 DT 06-04-2003 (first entry)
 DE Human GPCR polynucleotide SEQ ID NO 395.
 XX Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
 KM drug development; gustatory; taste; fragrance; gene; ds.
 KM Homo sapiens.
 OS WO200216548-A2.
 PN 28-FEB-2002.
 XX 30-JUL-2001; 2001WO-1B001446.
 XX 04-AUG-2000; 2000JP-00237818.
 PR 13-FEB-2001; 2001JP-00034434.
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA Haga T, Takeda S, Mitaku S;
 PI WPI; 2002-304118/34.
 DR P-PsDB; ABP95793.
 DR Database global search for G protein-coupled receptors, proteins and
 PT encoded genes for studying in vivo signal transduction mechanism and
 PT identifying targets for drug development.
 XX Claim 9; SEQ ID NO 395; 97pp + Sequence Listing; Japanese.

The invention relates to a method for screening G protein-coupled
 CC receptor (GPCR) genes (AB242870-AB243216) and/or GPCR proteins (ABP95596-
 CC ABP95962) by extracting open-reading frames containing 6-8 transmembrane
 CC domains with 250-1000 amino acid residues to give a gene homologous with
 CC a known GPCR gene. The receptor proteins and encoded genes are useful for
 CC studying in vivo signal transduction mechanism and identifying targets
 CC for drug development e.g. based on olfactory and gustatory receptors in
 CC form of agonists and antagonists by screening intrinsic and extrinsic
 CC ligands as bitter taste inhibitors, taste enhancers and fragrance
 CC improvers. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly

CC from WIP0 at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 933 BP; 192 A; 251 C; 188 G; 302 T; 0 U; 0 Other;
 Query Match 71.8%; Score 691.6; DB 6; Length 933;
 Best Local Similarity 84.0%; Pred. No. 8.1e-188;
 Matches 781; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

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 DB 4 GCACCAAAACCTTTCTGTGACAGAGTTATCTCGAAGCTTACCCAGCCGGA 63
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RESULT 14
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 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Human DNA for olfactory and pheromone G protein-coupled receptor #55.
 XX
 KW Human; ds; gene; olfactory and pheromone G protein coupled receptor;
 KW GPCR; tranquillizer; antidepressant; neuroleptic; endocrine; anabolic;
 KW anorectic; taste; fragrance; food additive; cosmetic; cell migration;
 KW sterility; psychotic disorder; neurological disorder; anxiety;
 KW schizophrenia; manic depression; depression; axonal growth;
 KW menstrual cycle; appetite sexual motivation; sexual attraction;
 KW aggression.
 KW
 OS Homo sapiens.
 XX
 PN W0200224726-A2.
 XX
 PD 28-MAR-2002.
 XX
 PF 21-SEP-2001; 2001WO-BE000162.
 XX
 PR 22-SEP-2000; 2000EP-00870211.
 XX
 PA (CHEM-) CHEMCOM SA.
 XX
 PI Veithen A;
 XX
 XX WPI; 2002-330013/36.
 DR P-PSDB; AAU95568.
 PT
 PT antagonists or inhibitors useful in food or cosmetic products or in the
 PT treatment or prevention of neurological disorders such as anxiety and
 PT schizophrenia.
 PS
 PS Disclosure; Page 178-179; 833pp; English.
 XX
 XX The invention relates to olfactory and Pheromone G-protein coupled
 CC receptor (GPCR) or a protein 95% identical to the GPCR, a specific active
 CC portion and its encoding polynucleotide. Also included are an agonist,
 CC antagonist or inhibitor of the GPCR or the polynucleotide, a vector
 CC comprising the polynucleotide, a cell transformed by the vector, a non-
 CC human mammal comprising a partial or total deletion of the polynucleotide
 CC encoding the receptor and screening (detection and possibly, recovering)
 CC of compounds which are known or not known to be agonist, antagonists or
 CC inhibitors of natural compounds to the GPCR. The receptor-derived
 CC agonists, antagonists, inhibitors or compounds are used as an
 CC improvement, elimination or substitution of an existing taste and/or a
 CC fragrance of (or in) the food and/or cosmetic products. They can also be
 CC used in the preparation of medicament in the treatment and/or prevention
 CC of a mammalian disorder, including anxiety, sterility, psychotic and
 CC neurological disorders, such as cell migration, sterility, psychotic and
 CC depression, depression, for promoting axonal growth, nerve cell
 CC connection and nerve regeneration for modulating male and female
 CC endocrine functions, hormone production and the menstrual cycle, for the
 CC prevention or the treatment by stimulation of several mammalian
 CC behaviours, such as stimulation or suppression of appetite, sexual
 CC motivation, sexual attraction, aggression and for promoting or
 CC suppressing chemical communication between organisms. The present
 CC sequence is a human DNA encoding an olfactory and pheromone GPCR
 XX
 XX Sequence 933 BP; 192 A; 251 C; 188 G; 302 T; 0 U; 0 Other;
 Query Match 71.8%; Score 691.6; DB 6; Length 933;
 Best Local Similarity 84.0%; Pred. No. 8.1e-188;
 Matches 781; Conservative 0; Mismatches 141; Indels 0; Gaps 0

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 29, 2004, 22:46:01; Search time 4162 Seconds
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Searched: 3470272 seqs, 21671516395 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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3	961.4	99.8	192926	9	AP000916 Homo sapi
4	960.4	99.7	994	6	AX241500 Sequence
5	755.4	78.4	931	6	AX646877 Sequence
6	751	78.0	935	6	AX241493 Sequence
7	694.2	72.1	991	6	AX702842 Sequence
8	694.2	72.1	1333	6	AB065834 Homo sapi
9	694.2	72.1	1333	9	AP001524 Homo sapi
10	694.2	72.1	150847	9	AP001524 Homo sapi
11	694.2	72.0	172991	2	AC083958 Homo sapi
12	693	72.0	976	6	AX555206 Sequence
13	692.4	71.9	953	6	AX554459 Sequence
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ALIGNMENTS

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DEFINITION Sequence 23 from Patent WO0250275.
ACCESSION AX555964
VERSION AX555964.1 GI:25899399
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Padigaru,M., Kekuda,R., Li,J., Ballinger,R.A., Caeman,S.J.,
Spytek,K.A., Baumgartner,J.C. and Burgess,C.E.
TITLE Novel proteins and nucleic acids encoding same

JOURNAL Patent: WO 0250275-A 23 27-JUN-2002;
 Curagen Corporation (US)
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Query Match 100.0%; Score 963; DB 6; Length 963;
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 Matches 963; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 LOCUS
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 HTG; HTG_PHASE1; HTG_DRAFT.
 KEYWORDS
 Homo sapiens (human)
 ORGANISM
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 Birren, B., Linton, J., Nusbaum, C. and Lander, E.
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 Strauss, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Turrell, A., Travers, M., Triggillo, J., Vasiliev, H., Viel, R., Vo, A.,
 Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,
 Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (08-OCT-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 2, 2001 this sequence version replaced gi:10717225.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

TITLE
 JOURNAL
 COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research
 Genome Center
 Web site: <http://www-seg.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: L11149
 Center clone name: 18 M 5
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DEFINITION Sequence 1069 from Patent EP1270724.
ACCESSION  AX646877
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REFERENCE   1
  AUTHORS   Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H.
  TITLE     Guanine triphosphate-binding protein coupled receptors
  JOURNAL   Patent: EP 1270724-A 1069 02-JAN-2003;
            National Institute of Advanced Industrial Science and Technology
            (JP) ; Center for Advanced Science and Technology Incubation, Ltd.
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Best Local Similarity 99.9%; Pred. No. 4,5e-181;
Matches 756; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION Sequence 241 from Patent WO0127158.
ACCESSION  AX241493
VERSION     AX241493.1  GI:15798368
KEYWORDS
SOURCE      synthetic construct
            artificial sequences.
ORGANISM
REFERENCE   1
  AUTHORS   Bellenson, J., Smith, D., Lancel, D., Guzman, G., Fuchs, T. and
            Yanai, I.
  TITLE     Olfactory receptor sequences

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 AX646099
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H.
 Guanine triphosphate-binding protein coupled receptors
 Patent: EP 1270724-A 291 02-JAN-2003;
 National Institute of Advanced Industrial Science and Technology
 (JIP) ; Center for Advanced Science and Technology Incubation, Ltd.
 (JIP)
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 Best Local Similarity 83.7%; Pred. No. 1.7e-165;
 Matches 786; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

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 AB065834
 ACCESSION AB065834.1 GI:21928933
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

1 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
Suwa, M., Sato, T., Okouchi, I., Arita, M., Futami, K., Matsunoto, S.,
Tsubota, S., Aburatani, H., Asai, K. and Akiyama, Y.
Genome-wide discovery and analysis of human seven transmembrane
helix receptor genes
Unpublished
2 (bases 1 to 1333)
Suwa, M.

Direct Submission
Submitted (11-JUN-2001) Makiko Suwa, Computational Biology Research
Center (CBRC), National Institute of Advanced Industrial Science
and Technology (AIST); 2-41-6 Aomi Koto-Ku, Tokyo 135-0064, Japan
(E-mail: m-suwa@aist.go.jp, URL: http://www.cbrc.jp/
Tel: 81-3-3599-8080, Fax: 81-3-3599-8081)
This sequence is a seven transmembrane helix receptor candidate
predicted from the whole human genome sequences using our automated
system that contains programs of gene
finding (GeneDecoder), sequence search, motif-domain assignment and
transmembrane helix prediction.
And the sequence is submitted by the collaborative project between
(Computational Biology Research Center (CBRC), National Institute
of Advanced Industrial Science and Technology (AIST)) and (Genome
Science Division, Research Center for Advanced Science and
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ORIGIN

Query Match 72.1%; Score 694.2; DB 9; Length 1333;
Best Local Similarity 83.7%; Freq. No. 1.7e-165;
Matches 786; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

8 GCCGAGAACTCTCTCCGACAGAGTTATCTCGAGGCTTAATCCACGCGGGA 67
204 GAGCGAATAAATCTCTGTCGACAGAGTTATCTCGAGGCTTAATCCACGCGGGA 263
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DB 564 TAGTGGGATCTGTAAACCACTGTGTACAGATACCAATGTCCTCCAGGNGTTTG 623
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complete sequence.
ACCESSION AP001524
VERSION AP001524.4 GI:15320470
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Published Only in Database (2000)
2 (bases 1 to 150847)
REFERENCE
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: hattori@sc.riken.go.jp, URL: http://hgp.riken.go.jp/
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT On Aug 27, 2001 this sequence version replaced gi:9798616.
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ACCESSION
VERSION
KEYWORDS
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ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

TITLE	JOURNAL	COMMENT
1. The Role of the State in Economic Development	Journal of Economic Surveys	See also [1] for a related discussion.
2. The Impact of Globalization on the Labor Market	Journal of International Economics	See also [2] for a related discussion.
3. The Effect of Trade Policy on the Environment	Journal of Environmental Economics	See also [3] for a related discussion.
4. The Role of the State in the Provision of Social Insurance	Journal of Public Economics	See also [4] for a related discussion.
5. The Impact of Fiscal Policy on the Labor Market	Journal of Public Economics	See also [5] for a related discussion.
6. The Effect of Trade Policy on the Environment	Journal of Environmental Economics	See also [6] for a related discussion.
7. The Role of the State in the Provision of Social Insurance	Journal of Public Economics	See also [7] for a related discussion.
8. The Impact of Fiscal Policy on the Labor Market	Journal of Public Economics	See also [8] for a related discussion.
9. The Effect of Trade Policy on the Environment	Journal of Environmental Economics	See also [9] for a related discussion.
10. The Role of the State in the Provision of Social Insurance	Journal of Public Economics	See also [10] for a related discussion.

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AC083958.2 GI:13184080
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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Birken,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome, clone RP11-18W5
Unpublished
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Birken,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Barina,N., Bassett,J., Bede,F., Boguslavsky,L.,
Boukhalter,B., Brown,A., Burkett,G., Campoliano,A., Castle,A.,
Choepl,Y., Collangelo,M., Collins,S., Collymore,A., Cooke,P.,
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Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,T.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (30-OCT-2000) Whitehead Institute/MIT Center for Genome
Research, 130 Charles Street, Cambridge, MA 02141, USA
On Mar 2, 2001 this sequence version replaced gi:10717225.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: submissions@genome.wi.mit.edu
----- Project Information

Center project name: 11149
Center clone name: 18.M.5
----- Summary Statistics
Sequencing vector: Plasmid; n/a, 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; Version 0.960731
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Consensus quality: 170912 bases at least Q30
Consensus quality: 171602 bases at least Q20
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Insert size: 172291; sum-of-*contigs*
Quality coverage: 7.3 in Q20 bases; agarose-*fp*
Quality coverage: 7.4 in Q20 bases; sum-of-*contigs*

* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 *contigs*. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the *contigs* are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

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 VERSION AX244609.1 GI:15859510
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 REFERENCE 1 Lal, P., Tang, Y.T., Patterson, C., Yao, M.G., Shih, J.L.,
 Tribouley, C.M., Lu, D.A., Yue, H., Khan, F.A., Policky, D.L.,
 Au-Yang, J., Yang, J., Harland, L., Walsh, R.T., Lo, T.P. and
 Borowsky, M.L.
 G-protein coupled receptors
 JOURNAL Patent: WO 0166742-A 35 13-SEP-2001;
 Incyte Genomics, Inc. (US)
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 QY 908 AGAACCTTTCCAGATAAGCTTTCTTAAATA 937
 Db 904 AGAACCTTTCCAGATAAGCTTTCTTAAATA 933
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 AX448443 933 bp DNA linear PAT 03-JUL-2002
 LOCUS Sequence 109 from Patent WO0224726.
 DEFINITION AX448443
 ACCESSION AX448443
 VERSION AX448443.1 GI:21697342
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 Veithen, A.
 Olfactory and pheromones g-protein coupled receptors
 JOURNAL Patent: WO 0224726-A 109 28-MAR-2002;
 ChemCom S.A. (BE)
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 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
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 /note="unnamed protein product"
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 /db_xref="GI:21697343"
 /db_xref="REFSEQ:CAD37543"
 /translation="MAKNSVTEFFLEGLTHPGRLRPLFLEFLGTYTVVGNGL
 ILLGLNSHLTPMVFLENLSLIDPCEFTTTPKMLSPVSRNIIISFGCTQLFP
 FCFEVSSEFSLAAAYDRVAICNPILYTVMSQVCLILLGAYMGFAGAAHTG
 SIMLTFCADLVNHFMDLPLLELSCNSYMEIVLVFVAVDVPMPVTVVISA
 LLSILHNSSTERSKAFSTCSGSHIIVLSFSGSAFVFLKPLSLPLSGKXSLF
 YTIIVPVLNPLIYSLRKDVAVLRLRLKRIFS"
 ORIGIN
 Query Match 71.8%; Score 691.6; DB 6; Length 933;
 Best Local Similarity 84.0%; Pred. No. 7,66-165;
 Matches 781; Conservative 0; Mismatches 149; Indels 0; Gaps 0;
 QY 8 GCGGGAAGTCTCTCTCGGTGACAGAGTTTATCTCGAGGCTTAATCCACCGCGGA 67

Db 4 GCAGCCAAAACCTCTTCTGTGACAGATTATCTCGAAGCTTACCACACAGCCGGGA 63
QY 68 CTCAGAGTCCCGCTCTTCTCTGTCTAGTCTTACGCGGTACCGGTGTGGGAAAC 127
Db 64 CTGGGAAATCCCGCTCTTCTCTGTCTGTGGGTCTACACGGTCAACGGTGTGGGAAAC 123
QY 128 CTGGGCTTGAATATCTGTATAGGGCTCACTCTGCTGCAATGCCATATCCCATCTTTTC 187
Db 124 CTGGGCTTGAATATCTGTATAGGGCTCACTCTGCAATGCCATATCCCATCTTTTC 183
QY 188 CCTTCACTGTCCCTGTAGATTATTTAGTTCTCTACAGACCATATCCCAAAATGCTG 247
Db 184 CTTTAACTCTCTTAAATAGATTCTGTCTTCTCCATACCATCATCCCAAAATGCTG 243
QY 248 ATGAGTTTGTCTCAAGAAAGACATTAATTCCTTCAAGGTTGTATGAGTCTTC 307
Db 244 ATGAGTTTGTCTCAAGAAAGACATTAATTCCTTCAAGGTTGTATGAGTCTTC 303
QY 308 TTCTTCTGTCTTCTTCTTCTTCTGTAGTCTTCACTGTGCGGAGATGTGAGAGCCGC 367
Db 304 TTCTTCTGTCTTCTTCTTCTTCTGTAGTCTTCACTGTGCGGAGATGTGAGAGCCGC 363
QY 368 TACGTGGGATCTGTAAACCACTGTGTACAGATCAACATGTCTCCCAAGTGTGTTG 427
Db 364 TACGTGGGATCTGTAAACCACTGTGTGTACAGATCAACATGTCTCCCAAGTGTGTTG 423
QY 428 CTCCTTTTACTGGGTGTCTACAGGATGGGGTTTGGGGCTGTGGCTATACAGGAAT 487
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QY 488 ATAGTGTCTACCTTTTGT 547
Db 484 ATAGT 543
QY 548 CCCCTTTTGT 607
Db 544 CCTTCTGT 603
QY 608 GTGACGTTGGGATGGGGT 667
Db 604 GTGACGTTGGGATGGGGT 663
QY 668 TCCAGCATCTCCGCTTAGT 727
Db 664 TCCAGCATCTCCGCTTAGT 723
QY 728 TCTTCAATATGTGAGTTCTTCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 787
Db 724 TCCCAATATATGT 783
QY 788 CCTTCAATATATCCCTGTGACAGGGAAGTGTCTCTGTGTGTGTGTGTGTGTGTGTGT 847
Db 784 CTTTCAATATATCCCTGTGACAGGGAAGTGTCTCTGTGTGTGTGTGTGTGTGTGTGT 843
QY 848 CCCATGTTTAAACCATTAATCTTACAGCTGTAGGAATTAAGATGTCAACTTGCCCTGAAG 907
Db 844 CCCGTTTAAACCATTAATCTTATAGCTGTAGGAATTAAGATGTCAAAAGTGTCCCTGAGG 903
QY 908 AGAAGCTTTTCCAGAAATAGCTTTTCTTGA 937
Db 904 AGAAGCTTTTGGCAAAAAATCTTTCTTAA 933

Search completed: September 30, 2004, 00:31:00
Job time : 4168 secs

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Db 126 CACCCTTCCCTCTTGAGCTCTGCAAGCGCTCTTACATAAATGCTGTCATCTT 67
QY 601 TATTGTTGACCGTTGGCATTTGGGATGGCCATTGTCGCCGTTTATCTCTTAAGTTT 660
Db 66 TATTGTTGACCGTTGGCATTTGGGATGGCCATTGTCGCCGTTTATCTCTTAAGTTT 8
QY 661 TATTCTT 667
Db 7 TATTCTT 1
RESULT 2
US-09-016-434-1114
Sequence 1114, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1114:
SEQUENCE CHARACTERISTICS:
LENGTH: 945 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1336040
US-09-016-434-1114
Query Match 27.5%; Score 265; DB 4; Length 945;
Best Local Similarity 56.0%; Pred. No. 4,3e-73;
Matches 502; Conservative 0; Mismatches 395; Indels 0; Gaps 0;

QY 14 AACTCTCTCTCCGAGAGAGTTATCTCGCAAGGCTTAATCCACCAAGCGGAGCTCCAG 73
Db 19 AACTACAGGTTGGCAGCATGAGTTATCTCTTAAGTTTCCAACTGCGCCCTGAACGCG 78
QY 74 GTCCCGCT 133
Db 79 ATTCT 138
QY 134 TTGATATCCGATAGGCGTCAACTCTGCGCTGATATCCCACTGTTTCCCTTC 193

Db 139 TTGATCTGTGATCAGAGATTGATCTCTCACTTCAACCCCATGATTTTTCCTTAC 198
QY 194 AACTGTCCTGATATTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 253
Db 199 AACTGTCCTGATATTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 258
QY 254 TTGTCCTCAAGAGAGACATTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 313
Db 259 TTCTCTCTGAGAGAACATTTCTATTTCTATTTAGGCTGTGCTGAGTTTATTTTCT 318
QY 314 TCTTTCTTTCT 373
Db 319 TGTACTTTGACAGATACAAATCTTCACTCTGCGCGCCATGCTATGATGCTATGTC 378
QY 374 GGCATCTGTAACCACTGTTGTACAGATCATCATCTCTCTCTCTCTCTCTCTCTCTCTCT 433
Db 379 GCGATCTGTAACCTTTATTTGACAGATGATGATCTCTCTCTCTCTCTCTCTCTCTCTCT 438
QY 434 TTAGTGGGTCTACGCGAGTGGGGTTTGGGGCTGTGCTCATACAGAAATATAGT 493
Db 439 ATTGCTTGTCAATCTCTGAGCAACATGATGTTCCCTGTTCAACATCTTCTCTCT 498
QY 494 TTCTGACCTTTGTGACAGACAACTGTGATCTCACTCATGTGTGATCTCTCTCTCTCT 553
Db 499 ATTCTGAATATTTGACAAATATTTATTTATTTCTCTGACCTCTCTCTCTCTCTCT 558
QY 554 GTTGAAGCTCTCTGCAAGCGCTTTTACATTAATGCTCTCTCTCTCTCTCTCTCTCTCT 613
Db 559 CTTAAACTATCTGACATGACACAAATTAATGAGTGGCTCTCTCTCTCTCTCTCTCTCT 618
QY 614 GTTGGATTTGGGGTGGCATTTGTCCTTTTATCTCTTATGTTTATTTCTCTCTCTCT 673
Db 619 TTAGAGAAATATTTGTTTATCTATCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 678
QY 674 ATTCTCCGCTTGTCTGAGGAGGAGGTCTTAAGGCTTCAAGCTGACGCTCTCTCTCT 733
Db 679 GTCTTAAGATCCGCTCTTTTCAAGTGGAGAAAGACCTTTTCTCAATGGGCTCTCTCT 738
QY 734 ATTAATGCACTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTCT 793
Db 739 CTGACTTGAAGTACATCTTACCAAGGACTCTCTCTTTATTTATCTCAAGGCTCTCTCT 798
QY 794 ATTTAACCCTGACCAAGGAGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 853
Db 799 CIGTATTTCTCCAAACATGATTAATTTCTCAGTGTCTACACATTTTATTTCTCACTG 858
QY 854 TTAAACCATTAATCTACAGCTGTGAGATTAAGATGTCAAACTTGCCTGAAGAGA 910
Db 859 CTGAATCCGTTGATTTATGTTTGAATAATGAAGATGAAGATGACGTGAGAAA 915
RESULT 3
US-09-668-680-11
Sequence 11, Application US/09668680
Patent No. 6436703
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Wang, Jian-Rui
APPLICANT: Xue, Aidong J.
APPLICANT: Xu, Chongjun
APPLICANT: Dumanac, Radoje T.
TITLE OF INVENTION: No. 6436703el Nucleic Acids and
FILE REFERENCE: 790CIP2A
CURRENT APPLICATION NUMBER: US/09/668,680
CURRENT FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/540,217

; PRIOR FILING DATE: 2000-03-31
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: pt_FL_genes Version 2.0
 ; SEQ ID NO 11
 ; LENGTH: 1297
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (225)..(1091)
 US-09-668-11

Query Match 24.6%; Score 236.6; DB 4; Length 1297;
 Best Local Similarity 54.4%; Pred. No. 4,4e-64;
 Matches 476; Conservative 0; Mismatches 399; Indels 0; Gaps 0;

QY 60 AGCCGGAGCTCCAGTCCCGCTCTTCTTCTAGATTTCTACGGGCTACGGTGG 119
 DB 184 ATCCAGACTGCGAGCCAGTCTTCTGGGCTGTCTCTCATGTGCTGTCACGGTCC 243
 QY 120 TGGGGAACCTGGGCTTGAATATCTGATAGGGCTCACTGCGCTGATATCCCATGT 179
 DB 244 TGGGGAACCTGGCTCATCTCTGCGCATCAGCCCTGACTCCACCTCCACACCCCATGT 303
 QY 180 ACTTTTCCCTCACTGTCCCTGTAATTTTGTCTTCTAGACCATCATTCCTCA 239
 DB 304 ACTTCTCTCTCAACCTGTCTGCTGACATCGGTTTCACTTCCACCGGTTCCCA 363
 QY 240 AATGCTGATGAGTTTGTCTCAGAGAGACATTTTCTTCCACAGGGTGTATGATC 299
 DB 364 AGATGATTTGACATGCAAACTCAGAGAGATCATCTCTATGAAAGCTGCTGACTC 423
 QY 300 AGTTCTTCTTCTCTGTTTCTTGTCTTCTTCTGATGCTTCACTCTGCGGAGATG 359
 DB 424 AGATGCTTTTCTTGTCTTGTCTTGTGATGATGATGATGCTCCAGTGTGATGGCT 483
 QY 360 AGGACGCTACGTTGGGCTGATGTAACCACTGTTGTAACAGATCAACCATCTCCCCAG 419
 DB 484 ATATCCGGTTTGTGCGCATGTGCAACCCCTGCACTACCGAATCATATGAACCCAGCC 543
 QY 420 TGTGTTGCTCTTCTTACTGAGGTGTCTACGGAGTGGGGGTTTGGGGCTGTGCTCAT 479
 DB 544 TCTGAGCTCTTAATCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 603
 QY 480 CAGGAATATAGTCTTCTACCTTTTGGCAGACAACTCTGATCATCTCATATGCTG 539
 DB 604 ATTGATATGATACAGCTCAGCTGCTTCAAGATGTCATATTTCTTCTTCTG 663
 QY 540 ACATCTTCCCTCTTCTGAGCTCTCTGCAACGGCTCTTAATATATGCTGCTGATCT 599
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 QY 600 TTAATGTTGACCGTTGGGATGCGGATGCTGCTGCTGCTGCTTCTTCTTCTTCTTCT 659
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 DB 784 AATTTGTTTCCCATCTCTGAGAGTTCACATCATATGAGAGATTAAGCTTCTTCTCA 843
 QY 720 GCTGACACTCTCAATATGACAGTTTCTTCTTCTTGGGTCAGAGACTTTCATCTAC 779
 DB 844 CCTGTGCTCTCACTGCGAGTTGTTGCTTATTTATGGAACAGGAGCTTGTAGGGTAC 903
 QY 780 TCAACCCCTTCCATTTTACCCCTGAGACAGGAGGAGAGTCTCCCTGTTTATATCA 839
 DB 904 TCAATTAGCTGTGTTACATCCCAAGAGAGATGTTGCTTCAATGATATATCACTG 963
 QY 840 CTGTGTGCTCATTTTAACTTATATCTACAGCTGAGAGATTAAGATGTCAACTTG 899
 DB 964 TGTGACCCCATCTCAACCCCTTCACTACAGCTGAGAGATTAAGATGTCAAAGT 1023
 QY 900 CCTGAAGAGACCTTTTCCAGAAATAGCTTTCT 934

DB 1024 CCTGTGAGCTTCCATGCGAGATCATCAATCT 1058

RESULT 4
 US-09-016-434-1313
 ; Sequence 1313, Application US/09016434
 ; Patent No. 650938
 ; GENERAL INFORMATION:
 ; APPLICANT: Janice Au-Young
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 ; NUMBER OF SEQUENCES: 1490
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,434
 ; FILING DATE: HEREMITH
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0002 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1313:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1438 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GENBANK
 ; CLONE: 932092
 US-09-016-434-1313

Query Match 23.8%; Score 229.2; DB 4; Length 1438;
 Best Local Similarity 54.1%; Pred. No. 1e-61;
 Matches 490; Conservative 0; Mismatches 413; Indels 3; Gaps 1;

QY 11 GAGAACTCTCTCTCTGACAGATTTATCTCTGACAGCTTATATCCACAGCCGGAGCTC 70
 DB 371 GAGAACTTATCTCATCATGATGATTTTCTTCCAGAGTTCTTCTAGCTTCAAGAGAG 430
 QY 71 CAGTCCCT 130
 DB 431 CAGATCACCT 490
 QY 131 GCTTATATCT 190
 DB 491 ATCATTTGACATCATCT 550
 QY 191 TTCACCTTCT 250
 DB 551 AGCATGCTGCT 610
 QY 251 AGTTTGTCTCAGAGAGACATTAATTTCTTCAAGGGTATAGTCACTTCTTCTTCTC 310

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Db      611 AGCTCTGATGATGATGACCAAGCCAGTATGAGGAGGCTGGCCACAGATGTTCTTT 670
Qy      311 TTCTGTTCTTTGTTCTTTTCTGATCTTCATCTCTGCGCGATGAGAGCCGCTAC 370
Db      671 TTGTAACTTTGGATGACTAAGTCTCTGCTCAGAGCAATGGATATGACCGCTAT 730
Qy      371 GTGGGATCTTAAACCACTGTGTACAGATCACCAGTCTCCCCAGGTGTGTGCTC 430
Db      731 GTGGGATCTTGAACCCCTGAGATACATGTTATATGACAGAGGCTCGATCCAA 790
Qy      431 CTTTAACTGCTGTCTACAGGATGGGGGTTTGGGGCTGTGCTCATACAGAAATATA 490
Db      791 CTGTCTCTGGGGGCTGAGCAATGGGCTGATGTGAGCAATGACCAAGTACATCTTA 850
Qy      491 GTGTTTCACTTTTGTGACAGACAACCTTGCAATCACTACATGTGACATCTTCCC 550
Db      851 TTCAAGTTACCTTCTGTCTAGAAA---GGTCCCCACTTCTTGTGACATCGGCCCT 907
Qy      551 CTCTTGAAGTCTCTGACAGAGGCTTTACATATAATGCTCGATCTTTATTTGTGTG 610
Db      908 GTGATGAAGCTTCTCTGCAATGTACACACTGTCAATGAATCTGACTTGTATACGT 967
Qy      611 ACCGTTGGCATGGGGTGGCCATGTGCGGTTTATCTCTTATGTTTATTTCTTCC 670
Db      968 GTGCTGTCTGTTGTGACATAGGCTGTGTTTCATTTCTTATGTTCTATATCTCT 1027
Qy      671 AGCATTTCCGCGTATGTTTCTCTAGAGGAGGTAAAGCTTACAGTACGACGCTCC 730
Db      1028 ACAATCTCAAGATTTCACTGATGAGGCGGAGAAAGGCTTTTGCCACTGTGCACTC 1087
Qy      731 TACATATTCAGATTTCTTCTTTCTTGGATCAGAGCTTTTACGTAACCTCAAAACCCCT 790
Db      1088 CACTCAGCTGTGTATGTGACATGACAGCTGTGCTCATTTGCTTACTTCAAGCCAG 1147
Qy      791 TCCATTTTACCCTTGACAGGGAAGTGTCTCTCTGTTCTATCCACTGTGTGCTCC 850
Db      1148 TAGAGAAACACAGAAACATGACAGCTGATCTCGTGACCTACACTGTATCACTCCC 1207
Qy      851 ATGTTTAACTTATATCTACAGCTGAGAAATAGATGCAAACTTGCCCTGAGAGA 910
Db      1208 CTACTGAACCTGTGTATACCTGTGAATTAAGAGTCAAGATGCTGTGTGAGG 1267
Qy      911 ACCCTT 916
Db      1268 GCTGTT 1273

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; SEQ ID NO 10
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)..(1062)
US-09-668-680-10
Query Match      23.7%; Score 228.4; DB 4; Length 1062;
Best Local Similarity 52.8%; Pred. No. 1.5e-61;
Matches 493; Conservative 0; Mismatches 441; Indels 0; Gaps 0;

Qy      2 ATGCTGCGAGAACTCTCTCCGAGACAGATTTATCTGCGAGCTTATCCACCG 61
Db      124 ATGGAAGCAGAAACCAACAGAGATTTTGAAGTTATCTTCTGGAATCTGAGAT 183
Qy      62 CCGGAGCTCCAGATCCCGCTTCTCTGTTTCTAGTTTCTACGCGGTACAGGTG 121
Db      184 CCAAGACTACAGCGCTTCAATTTTGGGCTGTCTCTGTCAATGATCTGGGAGCGGTCTG 243
Qy      122 GGAACCTGGGCTTGATTAATCTGATAGGCTCAACTCTGCGCTGATATCCCATGAC 181
Db      244 GGAACCTGCTCATCACTCTGGCAATCAGCTGACTCCACCTCCACACCCCATGTAC 303
Qy      182 TTTTCCCTCAACTGTGCTCCGAGATTTTATGTTTCTTACAGACATATCCCAA 241
Db      304 TTTTCTCTTCAACTGTGCTCCGAGATTTTATGTTTCTTACAGACATATCCCAA 363
Qy      242 ATGCTGATAGTTTGTCTCAAGAAACATTAATTTCTTCAAGGATGATGATG 301
Db      364 ATGCTGATAGTTTGTCTCAAGAAACATTAATTTCTTCAAGGATGATGATG 423
Qy      302 TTTCTTCTTCTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 361
Db      424 GTCTATTTCTCAAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 483
Qy      362 GACCGCTACGTGGGCACTGTAAACCACTGTGTACAGATCAGATCAGATCTTCCAGGTG 421
Db      484 GACCGCTTGTGGCTGTGTGACACCTGTGCACTATGATCATGATGATGATGATGATG 543
Qy      422 TGTTCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 481
Db      544 TGTGGCTCTCTGTTTGTGCACTGTGCTATGATGATGATGATGATGATGATGATG 603
Qy      482 GGAATATAGTGTCTCACTTTTGTGAGACAACTGTGATCAATCAATCAATGATGATG 541
Db      604 TCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 663
Qy      542 ATCTTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 601
Db      664 CTGACGTACATCTCTCAGCTGCTGCTCTGATACCTTCTGAAACAGACAGCTGATATAC 723
Qy      602 ATTTGTTGACAGTTGGCATTTGGGGTGGCCATTTGTCGCTTTTATCTTATGCTTTT 661
Db      724 TTTATGACGGGTGTGTGTGGGCTTTTTCCTCTCTGAGATCATTTTCTTATTCACGA 783
Qy      662 ATCTTCTTCAAGATTTCTCGCGTTAGTTCTGTGAGGAGGAGCTTAAAGCTTCAATGAC 721
Db      784 ATGCTTATCATATAGGAAGATGCTCATCTGTGGGGAAGAAACAAAGACATTTCCACC 843
Qy      722 TGAAGTCTTATATATGCAATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 781
Db      844 TGTGGGCTCAGCTCTCTGCTGTTCTTATTTATGAGACAGGAGATGAGGCTTCCATTC 903
Qy      782 AAACCCCTTCCATTTTACCCCTGAGACAGGGAAGTGTCTCTCTCTTCTTATACACT 841
Db      904 ACTTGTGGGGTATGATCACTCTTCCAGAAATATCTCGTGGCTGTGATGATGATGATG 963
Qy      842 GTGATGCCATGTTTAAACCATTAATCTTACAGCTGAGGAATAGAGATGCAACTTGGC 901
Db      964 GTCAACCCCATGTTAAACCCCTTCAATCAAGCTGAGGAACAGAGATGAGAGGAGCC 1023

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RESULT 5
US-09-668-680-10
; Sequence 10, Application US/09668680
; Patent No. 6436703
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong Ju.
; APPLICANT: Xu, Chongjun
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6436703el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 790C1P2A
; CURRENT APPLICATION NUMBER: US/09/668,680
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 08/540,217
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: pt_fl_genes Version 2.0

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QY 902 CTGAGAGAACCTTTTCCAGAAATAGCTTTCTT 935
DB 1024 CTGGGAGTCTCTCTGACGAGGACGCTTCTT 1057

RESULT 6
US-09-016-434-1312
Sequence 1312, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1312:
SEQUENCE CHARACTERISTICS:
LENGTH: 1854 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g32085
US-09-016-434-1312

Query Match 23.6%; Score 227.2; DB 4; Length 1854;
Best Local Similarity 53.3%; Pred. No. 5e-61;
Matches 478; Conservative 0; Mismatches 418; Indels 0; Gaps 0;

QY 21 CCTCCGAGACAGATTATCTGCGAGGCTTAATCCACCGCCGGGAGTCCAGTCCCG 80
DB 339 CAGACATCTCAGACTTCTGCTCTCTGCGCTGCGCATCCACGACGAGCAAAACCTGT 398
QY 81 TCTTCTTCTGTTTCTAGTTTCTACGCGGTGAGGTGAGGAACTGAGCTTGATA 140
DB 399 GCTATGCCCTGTTTCTTGGCATGATTTATACACCCCTCGGGGAACTCTCATATG 458
QY 141 TCTGATAGGAGCTCACTCTGCGCTGATATCCCATGATCTTTCCCTTCACTGT 200
DB 459 TCTCATTCAGACTGATCCCATCTCCACAGCGCTTATGTTTCTTCCAGACCTGT 518
QY 201 CCCCGTATGATTTAGTTTCTCTAGACCATCATTTCCCAAAAGCTGATGTTTGTCT 260
DB 519 CCTTCTGACCTCTGCTTCTTCTCCGTGACCATTTCCAAAGTTGTTACAGAAATGACA 578

QY 261 CAGGAGAAATATTTCTTCAAGAGGTGATGATGATGATTTCTTCTTCTTCTTCT 320
DB 579 ACAGAGACCATCATCTCCCTATGCGGAGTGCATGCCAAATGATCTTCTCTGTTAT 638
QY 321 TTGCTTTTCTGAGTCTTATCTGCTGCGGAGTGGAGGAGACCGGTACGTGGGACT 380
DB 639 TTGAGACCTGAGAGGTTCTCTCTTGTGGCCAGGCTTATGACCGCTATGTCGCACT 638
QY 381 GTAACCATGTTGTATACCATCATCCATGCTCCCAAGTGTGTCTTCTTTACTGG 440
DB 699 GCTTCCCGCTGACTATACCGGCATATGAGCCCATGCTCTGCTGCTGCTGCTGCTG 758
QY 441 GTGTCTACGGATGAGGAGTTTGGGGCTGTGCTCTATAGGAATATGTTGTCTCA 500
DB 759 TGCTCGGTGCTGACCACTTCATGCAATGTTACACTTTACTCATGCGAGGTTGT 818
QY 501 CCTTTGTGAGACACTTGTCAATCATCATCATCATCATCATCATCATCATCATCATCAT 560
DB 819 GTTTTGTGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 878
QY 561 TCTCTGCAAGGCTCTTATCAATAATGCTCTGCTATCTTTATGTTGTGACCGTGGCA 620
DB 879 TGCCCTTCTGACATCGAGTTATGATGATGATGATGATGATGATGATGATGATGATGAT 938
QY 621 TTGGGAGCCCATGTTGCGGTTTATCTTATGTTTATCTTATCTTCTTCTTCTTCTTCT 680
DB 939 TTGATATCCATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 998
QY 681 GCGTTAGTTCTGCTGAGGAGGAGGCTTAAAGCTTCACTAGTGCAGCTCTTCAATAATG 740
DB 999 AGGTCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1058
QY 741 CAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 800
DB 1059 TGGTGTACATGTTCTTATGGAACGTTATGTTCTTCTTCTTCTTCTTCTTCTTCTT 1118
QY 801 CCTGAGACGAGGAGAAATGCTCTCTCTGTTCTTATACACTGTGAGTCCCATGTTTACC 860
DB 1119 CTACTCTTAAAGACATGCTATGCTATGATGATGATGATGATGATGATGATGATGAT 1178
QY 861 CATTATCTACAGCTTGAAGATTAAGATGTTCAACTTCCCTGTAAGAACCTTT 916
DB 1179 CCTTCACTACAGCTTGAAGATTAAGATGTTCAACTTCCCTGTAAGAACCTTT 1234

RESULT 7
US-09-668-680-9
Sequence 9, Application US/09668680
Patent No. 6436703
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
APPLICANT: Asundi, Vinod
APPLICANT: Wang, Jie
APPLICANT: Zhang, Jian-Rui
APPLICANT: Xue, Aiding J.
APPLICANT: Xu, Chongjun
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6436703el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 790C1P2A
CURRENT APPLICATION NUMBER: US/09/668,680
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
SOFTWARE: pc_fl_genes Version 2.0
SEQ ID NO 9
LENGTH: 1080
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (178)..(1080)
US-03-668-680-9

Query Match 23.5%; Score 226.6; DB 4; Length 1080;
Best Local Similarity 53.1%; Pred. No. 5.5e-61;
Matches 481; Conservative 0; Mismatches 424; Indels 0; Gaps 0;

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QY 30 CAGAGTTATCTCGAGGCTTAATCCACACCGCGGACTCCAGGTCCTCCCTCTTCTTC 89
DB 107 CAGAAATCCCTCTCTCGGAGCTCTCAGAGATCCAGAACTGAGCCCTCTCCCTGAGC 166
QY 90 TGTTCCTAGGTTCTACGGGCTGACGGGTGGTGGGAACCTGGCTTGAATCTGATAG 149
DB 167 TCTCCTCTCCATGATCTGCTGACGGGTGAGGAGAACCTGCTATCCTCGCTGCA 226
QY 150 GGCCTCACTGCGCTGCTGATATCCCATGATCTTTTCCCTTCACTTGTCCCTGAG 209
DB 227 GCTTGACTCCACCTCCACACCCCATGCTGCTTCTTCTCCATCCAACTGTGCTGGGCTG 286
QY 210 ATTATAGTTCTCTACGACATCATCTCCCAAAATGCTAGTGTCTCAAGAGAGA 269
DB 287 ACATCGGTTTCACTCGGCAATGCTCCCAAGATGATGAGATGAGATGAGATGCA 346
QY 270 ACATATTTCTCTCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 329
DB 347 GAGTCATCTCTTATGCGGGCTGCGCTGACAGAGATGCTTCTTCTGCTTCTTCTGATGA 406
QY 330 CTGATCTCTTATCTCTGCGGATGCTGAGAGACCGCTAGCTGGGATCTGTAACCCAC 389
DB 407 TAGAAGACATGCTCTGACAGTGAAGGCTTATGACCGATGTTGCTGCTGCTGCTGCTG 466
QY 390 TGTTCATACATCAACATCAATCTCCAGGCTGCTGCTTCTTCTGCTGCTGCTGCTGCT 449
DB 467 TGCATCTACCATCTCAATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 526
QY 450 GGATGGGGGTTTGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 509
DB 527 TCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 586
QY 510 CAGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 569
DB 587 AGAATGAGAAATCTCCATTTTGTCTGAGCCATCTCAACTCTCAACTCTGCTGCTGCT 646
QY 570 ACGGCTCTTACATAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 629
DB 647 CTGACAGTCTATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 706
QY 630 CCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 689
DB 707 CCAATTCAGGATCTCTTGTCTTACGCTAACAATGCTCCCTCAATTCAGATTTTCAT 766
QY 690 CTGCTGAGGAGGCTCTAAAGCTTACAGTCTGAGCTCTTACATATGAGATTTCTC 749
DB 767 CATAGATAGGAATCTTAAAGCTTCTTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 826
QY 750 TTTTCTTGGGCTCAGAGCTTTTACGTAAGTCAAAACCCCTTCAATTTTACCCCTGACC 809
DB 827 TATTTTATGGAACGAGGCTATGCGGTGTAAGCTGATGATGATGATGATGATGATGATGAT 886
QY 810 AGGGAAGAGTCTCCCTCTCTTCTTATACAGTGTGAGGCTTAAATCCCATTTATCT 869
DB 887 ATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 946
QY 870 ACAGCTGAGGAATGAGATGCTCAACTTGGCTGGAAGAGAACTTTTCCAGATATGCT 929
DB 947 ACAGCTGAGGAATGAGGAATGCAATGCAAGTGGCTGTGAGAGCTGCGAGAGAAAGTGTG 1006
QY 930 TTTCT 934
DB 1007 AATCT 1011
```

RESULT 8
US-08-748-506-8
Sequence 8, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Rometic et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voigt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 03-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-748-506-8

Query Match 22.7%; Score 218.4; DB 3; Length 966;
Best Local Similarity 52.1%; Pred. No. 1.9e-58;
Matches 486; Conservative 0; Mismatches 446; Indels 0; Gaps 0;

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QY 11 GAGACTCTCTCTCCGTGACAGATTTATCTCGAGGCTTAATCCACACCGGAGCTC 70
DB 28 GAGAAATGTTGTCTGCAACGTTTTCATTTGCAAGTTCTGAGTCTCCGAGAA 87
QY 71 CAGTCCCGCTTCTCTCTGTTCTAGTTTCAAGCGGTCACGGTGGGGAACCTG 130
DB 88 TGTCTCTCTGTTTACCTTATCTCTATGTTCTTATGATGATGATGATGATGATGATGAT 147
QY 131 GCGTGAATATCTGATAGGCTCACTGCTGCTGATATCCCATTTTCTTCCC 190
DB 148 CTCATAGCCCTGCTATTTGTAACGTCATCTTACACACCCCATGATCTTCTTCTG 207
QY 191 TTCACCTTCCCTGCTGATTTTATGTTCTCTACGACATCATCTCCCAAAATGCTAGT 250
DB 208 GCGAATCTGCTCTCTGAGATGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 267
QY 251 AGTTTGTCTCAGAGAGAACATTAATTTCTTCAAGGCTGATGATGATGATGATGATGAT 310
DB 268 AGCTTGTGAGTGAAGCCCGAGAGATCTTTCAGGTGGGATGCGCACACAGATGTTTTC 327
QY 311 TTTCTTTCTTCTTCTTCTTCTGAGGCTTATCTCTGCTGCGGATGAGTGAAGACCGCTAC 370
DB 328 TTTATATTTCTTGTATTAATGAGTGTGCTTATTTGAGGCTGAGGCTTTGACCGCTAT 387
QY 371 GTGGCATCTGTAACCACTGTTGATACAGATCAACATGTCCTCCCAAGTGTGTTGCTC 430
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Thu Sep 30 08:53:36 2004

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Page 7

Db 388 ATGGGATATATGTTCCCACTCCATATGCAACCCGAATGAGCGTAGATATGCCCCAC 447
Qy 431 CTTTACTGAGGTGTCTAGCGGATGGGGGTTTGGGGCTGAGGCTATACAGGAATATA 490
Db 448 TTGGCAATGTTTCAATGGGTGATGGATGATGATGATGATGATGATGATGATGAT 507
Qy 491 GTGTTCTCACTTTTGTGTCAGACAACTTGTCACTCACTACATGATGATGATGATGAT 550
Db 508 TTCTCTTAACTTCTGTGAGCCCTGTGATGATGATGATGATGATGATGATGATGAT 567
Qy 551 GTTCTTGAAGCTCTCTGCAAGGCTCTTATGATTAATGATGATGATGATGATGATGAT 610
Db 568 CTCTGAGCACTTGGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 627
Qy 611 ACCGTTGAGTGGGGTGGCCATGTTGGCTTTTATCTTATGATGATGATGATGATGAT 670
Db 628 GTCTCTGATATCTAGCCCTTTTGTGATCATTATCTTATGATGATGATGATGATGAT 687
Qy 671 AGCATTTCCGGGTAGTTCTGCTGAGGAGGCTTAAAGCTTCACTGATGATGATGATGAT 730
Db 688 GCAGTCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 747
Qy 731 TACATATGCACTTCTCTTTCTTTGGGTGAGAGCTTTAGAGTCAAGCTCAAGCCCT 790
Db 748 CACCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 807
Qy 791 TCCATTTACCCCTGAGCAAGGGAAGTCTCTCCCTGTTTATACCACTGTGATGATGAT 850
Db 808 TCTAGCACTCAACAGAAATGACAAACTTGGCCCTCTTCTACACAGATGATGATGAT 867
Qy 851 ATGTTTAACTTATATCTACAGCTGAGGATGATGATGATGATGATGATGATGATGAT 910
Db 868 ATGTTTAACTTATATCTACAGCTGAGGATGATGATGATGATGATGATGATGATGAT 927
Qy 911 ACCTTTCCAGTAATAGCTTTCTGAAAAA 942
Db 928 ATTCTGACCTGAAAAAATTCTGTCAATTA 959

RESULT 9
US-09-016-434-1413
Sequence 1413, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Jennifer A. Young
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1413:
SEQUENCE CHARACTERISTICS:
LENGTH: 1282 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9516319
US-09-016-434-1413

Query Match 22.7%; Score 218.2; DB 4; Length 1282;
Best Local Similarity 52.9%; Pred. No. 2,7e-58;
Matches 469; Conservative 0; Mismatches 418; Indels 0; Gaps 0;

Qy 25 CGTACAGATTATCTCGAGGCTTAATCCACAGCCGAGACTCCCGCTT 84
Db 191 CATGCTGATGATCTCTGCTGAGGCTTCTGAGGCGCAGGCTGACGATGCTT 250
Qy 85 CTTCCTGTTCTAGGTTTCTACGGGCTACGGGTGAGGAGGAGGAGGAGGAGGAGGAGG 144
Db 251 TGCTCTCTCTCTTGTGCTACCTGATGATGATGATGATGATGATGATGATGATGAT 310
Qy 145 GATAGGCTCACTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 204
Db 311 TGCTGATGAGGCAAACTCCACACCCCATGATCTTCTCTGAGGAACTATAGT 370
Qy 205 CGTATATTATGTTCTCTACAGCATCATCCAAATGCTAGATGATGATGATGATGATGAT 264
Db 371 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 430
Qy 265 GAGAAATATTTCTCTACAGGAGGATGATGATGATGATGATGATGATGATGATGAT 324
Db 431 CAAGCTGACAGTCTCTGAGGAGGCTCTTACCCAGCTCTCTCTCTCTCTCTCTCTCT 490
Qy 325 CTCTTCTGAGCTTCT 384
Db 491 TGAAGTGAAGTCT 550
Qy 385 CCACTGTTTGAACGATACCATGCTCTCCAGAGTGTCTCTCTCTCTCTCTCTCTCTCT 444
Db 551 GCCCTTACCTTACAGCAACCCGATGATGATGATGATGATGATGATGATGATGATGAT 610
Qy 445 CTACGAGATGGGGGTTTGGGGCTGAGGCTTATACAGGAATATGATGATGATGATGAT 504
Db 611 CTGGCTGTGCTTACCAAGCACTGACCACTGAGGCTGAGGCTGAGGCTGAGGCTGAG 670
Qy 505 TTGTCAGACAACTTGTCACTCACTACATGATGATGATGATGATGATGATGATGATGAT 564
Db 671 CTGTGAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 730
Qy 565 CTGACAGGCTCTTATATATATGCTGTGATCTTTATGATGATGATGATGATGATGAT 624
Db 731 CTGCTCCAGCAACCACTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 790
Qy 625 GGTGCCCATGTTGGCGTTTATATCTTATGATGATGATGATGATGATGATGATGATGAT 684
Db 791 TACCCCATGCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 850
Qy 685 TAGTCTGCTGAGGAGGCTTAAAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 744
Db 851 TCGCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 910
Qy 745 TTCTCTTTTCTTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 804
Db 911 TGCCATATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 970
Qy 805 GGACGAGGGAAGTGTCT 864

Db 971 AGACAGAGATTAAGCTGTGGAAATTTCAACACTGTCTCATCATCCATGCTGACCCCAAT 1030
Qy 865 AATCTACAGCTTGAGAAATTAAGATGCTAACTGCGCTGAAGAGA 911
Db 1031 CATCTACAGCTTGAGAAACCTGATGTGAGAGTGCATCTGAGAGA 1077

RESULT 10
US-08-827-291A-1
; Sequence 1, Application US/08827291A
; Patent No. 5874243
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Sathie, Ganesh
; TITLE OF INVENTION: NOVEL OLRCIS RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: PA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,291A
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: GP50001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5015
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-827-291A-1

Query Match 21.9%; Score 210.6; DB 2; Length 1290;
Best Local Similarity 51.9%; Pred. No. 6,6e-56;
Matches 474; Conservative 0; Mismatches 439; Indels 0; Gaps 0;

Qy 2 ATGCTGCCGAGAACTCTCTCCGTGACAGAGTTTACTCGAGGCTTAATCCACAG 61
Db 296 ATGCGAAGGAGAAATTCGACCTTCACTCCGACTTCATCTTCCGGGAAATCTTCAATCAC 355
Qy 62 CCGGGAATCCAGTCCCGCTTCTCTCTGTTTCTAGATTTCACGGGGTCAAGGGTGG 121
Db 356 AGCCCAACCCACACACTTCTCTTCTTCTGCTGCGCAATCTTTTAGGGCTTCATG 415
Qy 122 GGAAGACTGGGCTTGATTAATCTGATAGGGCTCAACTCTGCGCTCATATCCCATGTAC 181
Db 416 GGAAGCTCTGATGATGTTCTCTCATCTACCTGACACCCAGCTCCACACCCCATGTAC 475
Qy 182 TTTTCCCTTCAACTGTGCTGCTGATTTTATAGTTTCTTCAAGCAATATTCCTCCAA 241
Db 476 CTCTCTCTCAACCACTGTCTCTTATGAGCTTCACTGCTCACTGACCACTGATCCAG 535
Qy 242 ATGCTGATGATTTTGTCTCAAGAGAACATATTTCTTCAAGGGTGTATGATGAC 301

Db 536 ATGACCTTCAACTACCTGTCTGACAGAGTCCATTTCTATGCTGTGTGCCACAA 595
Qy 302 TTTCTTCTTCTGTTTCTTCTTCTTCTTCTGAGTCTTCACTGTGTGGAGTGGAG 361
Db 596 ATTTCTTCTTCACTACTGCTTGGCTGTGAATGCTTCTTCTTCTTCTTCTTCTTCT 655
Qy 362 GACGCTACGTGGGCACTGTGAACCCACTGTGTGACAGATCAATGCTCCCAAGT 421
Db 656 GACGCTACACTGCACTGCAATTTGCCACCTTAAGATACCAATCTCATGAGCCCTAAAT 715
Qy 422 TGTTCCTCTTCTTCTTCTGAGTGTCTACGGGATGGGGGTTTGGGCTGTGCTTACA 481
Db 716 TGTGACTTATGACTGCTTCTTCTGATCTGGGCTGTACAGATGAATCAATTAATGCT 775
Qy 482 GGAATAATAGTGTCTTCACTTTTGTGAGACAACCTTGTCAATCACTACATAGTGTAC 541
Db 776 GTAGCCACATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 835
Qy 542 ATCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 601
Db 836 TTAACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 895
Qy 602 ATGTGTGACCGTGGCAATGGGGGCGCCATTTGCTTCTTCTTCTTCTTCTTCTTCT 661
Db 896 ATTTGCTCTATAGTATGCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 955
Qy 662 ATCTTCTTCAAGATTCCTGCGGTTAGTGTCTGAGGCGAGCTTAAGACCTTCAGTAC 721
Db 956 GTATTTCTGCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1015
Qy 722 TGCAGCTCCATATAATGCAATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 781
Db 1016 TGTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1075
Qy 782 AAACCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 841
Db 1076 CAGCCACATGTGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1135
Qy 842 GTGTGCTCCATGTTTAACCAATTAATCTTCAAGCTTGAAGAAATGAAGTCAAACTTGC 901
Db 1136 CTCACCTCCATGCTAATTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1195
Qy 902 CTGAAGAGAACT 914
Db 1196 TTCAAGAAATCT 1208

RESULT 11
US-09-546-986A-1
; Sequence 1, Application US/09546986A
; Patent No. 6635741
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. 6635741e1 G-Protein Coupled Receptors
; FILE REFERENCE: 018781-004720US
; CURRENT APPLICATION NUMBER: US/09/546,986A
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 09/524,730
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (42)..(974)
; OTHER INFORMATION: human breast cancer amplified G-protein coupled

OTHER INFORMATION: receptor 1 (BCA-GPCR-1)
US-09-546-986A-1

Query Match 21.8%; Score 210.2; DB 4; Length 1035;
Best Local Similarity 52.0%; Pred. No. 7,7e-56;
Matches 470; Conservative 0; Mismatches 433; Indels 0; Gaps 0;

22 CTCGAGACAGATTATCTCGACAGGCTTAATCCACAGCCGGGACTCCAGTCCCGT 81
53 CTCCTTAAGACCTTCACTCTGAGGTGTCTGACAGGCGGTGGTGAATCCCTCT 112
82 CTTTCTCTCTTCTTCAAGTTTCAAGCGGTCAAGTGTGGGGAACCTGGTGAAT 141
113 CTTTGTGCTCTCTGCTGCTTCTATGTGTGGCCAGTGTGGGAAGCTGGCATCAT 172
142 CCGATAGGGCTCAACTCTGGCTGCAATCCCAATGACTTTTCCCTTCACCTGTC 201
173 GGCATCCCGGTGATGCTTCACTCCACAGCCCAATGATCTTCTCAGTCACTGTC 232
202 CCGTGAATTTTGAATTTCTCTTCAAGCAATCAATCCCAAAATGCTGATGATTTGTC 261
233 CTTCTGAGACTCTGCTACACACACAGAGTCCCTCAGATGCTGCTACATGGGAG 292
262 AAGGAAGAATTAATTTCTTCAAGGGGTATGAGTCACTTCTTCTCTGTTTCT 321
293 TTCCCAAGAAACCATGACTATGAGAGCTGCACTGTGCAATATGCACTTCCACTGGCT 352
322 TGTCTTTTCTGAGTCTTCACTCTGTGGCGATGTGAGAGACCGCTACGTGGGATCTG 381
353 GGGATGACAGAGTGCATGCTCTGCGCCAGTGGCCGCTGGAACCGCTACGTGGGAGCTG 412
382 TAACCACTGTGTATACCATACCACTGTCTCCCAAGTGTGTGCTCTTTACTGGG 441
413 CAAGCCCTGCACTATGCTGCTCAAGACCTGTCTCTGTGACAGAGCTGTGGCTT 472
442 TGTCTACGGGATGGGGGTTTTTGGGGCTGTGCTCAATAGGAATAATATGTCTCA 501
473 GGGCTGCTCAAGTGTCTGAGCAACCTCTGCGAGGTGTGCTGACGATGCAATGTC 532
502 CTTTGTGACAGAACCTTGTCAATCACTAATGTGTGATCTTCCCTCTTGTAGCT 561
533 ATCTGAGGGGCGGAGGTGTGAACAATTTTCTGTAGGTGTGCGCGGTATCAAGCT 592
562 CTCTGCAAGGCTCTTACATTAATGCTGATCTTATGTGTGACGTTGGCAT 621
593 GTGTGTGCTGACACCGCTATGAAATGACATACCTGCTGTGTGTGTGTGTGTGTGT 652
622 TGGGGTGGCCATTTGTGCGGTTTTTATCTTATGTGTGTGTGTGTGTGTGTGTGT 681
653 GTGTGTGCTGCTGCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 712
682 CGTTATGTTCTGAGAGGAGGTCTTAAGGCTCAGAGCTGAGCTCTCTCTCTCTCTCT 741
713 GATCACTGCTCAAGGAGGACACAGAGCTTTGGAGCGTGTCTCTCTCTCTCTCTCT 772
742 AGTTTCTCTTTCTTGGTCAAGAGCTTTTACGTAACCTCAACCCCTCTCTCTCTCT 801
773 CGTCTCTCTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 832
802 CCGGACCAAGGGAAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 861
833 CCAAGACAGGGGCAATTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 892
862 ATTATATACAGCTGAGAAATAGATGATCAAACTGCGCTGAAGAACTTTTCAAG 921
893 CTTCACTACACCTCTGAAATATAGATATAGAGGGGCTCTGAGAGAACTTCTGGCAG 952
922 AAT 924
953 GAT 955

RESULT 12

US-09-524-730-1
Sequence 1, Application US/09524730
Patent No. 6638733
GENERAL INFORMATION:
APPLICANT: Powers, Scott
APPLICANT: Yang, Jianxin
APPLICANT: Cutler, Gene
APPLICANT: Tularik Inc.
TITLE OF INVENTION: No. 6638733el G-Protein Coupled Receptors
FILE REFERENCE: 018781-004710US
CURRENT APPLICATION NUMBER: US/09/524,730
CURRENT FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1035
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (42)..(974)
OTHER INFORMATION: human breast cancer amplified G-protein coupled
OTHER INFORMATION: receptor 1 (BCA-GPCR-1)
US-09-524-730-1

Query Match 21.8%; Score 210.2; DB 4; Length 1035;
Best Local Similarity 52.0%; Pred. No. 7,7e-56;
Matches 470; Conservative 0; Mismatches 433; Indels 0; Gaps 0;

22 CTCGAGACAGATTATCTCGACAGGCTTAATCCACAGCCGGGACTCCAGTCCCGT 81
53 CTCCTTAAGACCTTCACTCTGAGGTGTCTGACAGGCGGTGGTGAATCCCTCT 112
82 CTTTCTCTCTTCTTCAAGTTTCAAGCGGTCAAGTGTGGGGAACCTGGTGAAT 141
113 CTTTGTGCTCTCTGCTGCTTCTATGTGTGGCCAGTGTGGGAAGCTGGCATCAT 172
142 CCGATAGGGCTCAACTCTGGCTGCAATCCCAATGACTTTTCCCTTCACCTGTC 201
173 GGCATCCCGGTGATGCTTCACTCCACAGCCCAATGATCTTCTCAGTCACTGTC 232
202 CCGTGAATTTTGAATTTCTCTTCAAGCAATCAATCCCAAAATGCTGATGATTTGTC 261
233 CTTCTGAGACTCTGCTACACACACAGAGTCCCTCAGATGCTGCTACATGGGAG 292
262 AAGGAAGAATTAATTTCTTCAAGGGGTATGAGTCACTTCTTCTCTGTTTCT 321
293 TTCCCAAGAAACCATGACTATGAGAGCTGCACTGTGCAATATGCACTTCCACTGGCT 352
322 TGTCTTTTCTGAGTCTTCACTCTGTGGCGATGTGAGAGACCGCTACGTGGGATCTG 381
353 GGGATGACAGAGTGCATGCTGTGCGCGCATGCGCTGAGCGCTACGTGGGAGCTG 412
382 TAACCACTGTGTATACCATACCACTGTCTCCCAAGTGTGTGCTCTTCTTACTGGG 441
413 CAAGCCCTGCACTATGCTGCTCAAGACCTGTCTCTCTCTCTCTCTCTCTCTCT 472
442 TGTCTACGGGATGGGGGTTTTTGGGGCTGTGCTCAATAGGAATAATATGTGTCTAC 501
473 GGCATCCCGGTGATGCTTCACTCCACAGCCCAATGATCTTCTCAGTCACTGTC 532
502 CTTTGTGACAGAACCTTGTCAATCACTAATGATGACATCTTCCCTCTTGTAGCT 561
533 ATCTGAGGGGCGGAGTGTCTGAAATGATGCTGTGTATGTGTGTGTGTGTGTGTGT 592
562 CTTCTGCAAGCTCTTCAATTAATGTCTGTGTATCTTATGTGTGTGTGTGTGTGTGT 621
593 GTGTGTGCTGACACCGCTATGAAATGACATACCTGCTGTGTGTGTGTGTGTGTGT 652
622 TGGGGTGGCCATTTGTGCGGTTTTTATCTTATGAGTTTATCTTCTTCAAGATTTGCT 681
653 GTGTGTGCTGCTGCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 712

QY 682 CGTTAGTCTGCTGAGGAGGCTGTAAGCCTTCACTAGTCTGAGTCTGCTTACATATTCG 741
DB 713 GATCCAGCTCTCCAAAGGAGACACAAAGGCTTTGAGAGTGTCTCTCCACCTGATGAT 772
QY 742 AGTTCTCTTTTCTTTGGTCCAGGAGCTTTTACGTCTCCAAACCCCTTCCATTTTAC 801
DB 773 CGTCTCTCTTCTTACTTACTTCTGATTTTCAATGATGATGAGAGGCTTCCAGCTACTC 832
QY 802 CCTGAGCAGAGGAGAAAGTGTCTCTCTCTGTTCTATACACTGTGTGCTCCATTTTAAACC 861
DB 833 CCAAGAGCAGAGGAGAAATTTATTTCTCTCTTCTATTCATATACCCCACTCTCATTC 892
QY 862 ATTAATCTACGCTGAGGATTAAGATGATCAACTGCTGAGAGAGAACCTTTTCCAG 921
DB 893 CTTCACCTACCTGAGAAATTAAGATTAAGAGGAGGCTGAGAGAGCTTCTGAGCCAG 952
QY 922 AAT 924
DB 953 GAT 955

RESULT 13
US-08-748-506-5
; Sequence 5, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Ronnelt et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voigt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 966 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-748-506-5

Query Match 21.6%; Score 208.4; DB 3; Length 966;
Best Local Similarity 51.4%; Pred. No. 2.7e-55;
Matches 479; Conservative 0; Mismatches 453; Indels 0; Gaps 0;

QY 11 GAGAACTCTCTCTCCGAGAGAGATTAATCTCTGAGAGCTTAATCCACGAGCCGAGATC 70
DB 28 GAGAACTCTCTCTCCGAGAGATTAATCTCTGAGAGCTTAATCCACGAGCCGAGATC 87
QY 71 CAGGTCCCGCT 130

DB 88 TGCTTCT 147
QY 131 GGTCTGATTAATCTCTGATTAAGGCTCTCACTCTGAGCTGATATCCCAATGATCTTTCC 190
DB 148 CTATTAATCT 207
QY 191 TTCAATCT 250
DB 208 GCAACTGATCT 267
QY 251 AGTTTGTCTCAAGAGAAATTAATTTCTCTTCAAGAGGATGATGATGATGATGATGAT 310
DB 268 AGCTTGTGATGAGGCTCAAGAGATCTCTGAGAGAGATGATGATGATGATGATGATGAT 327
QY 311 TTCTGTTCT 370
DB 328 TTGCAATTTTCT 387
QY 371 GTGAGGATCTGATCCCACT 430
DB 388 ATGGCCATAGCT 447
QY 431 CTCTTACTGAGGATCT 490
DB 448 TTGCAATTTTCT 507
QY 491 GGTCTTCTCACT 550
DB 508 TTCTCTCTGAACT 567
QY 551 CTCTCTGAGCT 610
DB 568 CTCTCTGAGCT 627
QY 611 ACCGTGAGCTTGGGATGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 670
DB 628 GTCTCTGATTAATCT 687
QY 671 AGCATTTCTCGGATTAATCT 730
DB 688 GAGAGCT 747
QY 731 TACATTAATGAGCT 790
DB 748 CACCTACTGATGATCT 807
QY 791 TCCATTTTACCT 850
DB 808 TCTAGCACT 867
QY 851 AGTTTAACT 910
DB 868 ATGCTGAACT 927
QY 911 ACCTTTTCAGAAATTAAGCTTTTCTTGAAAAA 942
DB 928 ACTCTGGGCTGAAAAAATTTCTGCAATTA 959

RESULT 14
US-08-748-506-6
; Sequence 6, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Ronnelt et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voigt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US

ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-748-506-6

Query Match 21.5%; Score 207.4; DB 3; Length 966;
Best Local Similarity 51.3%; Pred. No. 5,6e-55;
Matches 4/8; Conservative 0; Mismatches 454; Indels 0; Gaps 0;

QY 11 GAGACTCTCTCCCTGACAGATTATCTCCGACGGCTTATACCAACCGCGGACTC 70
DB 28 GAGATAGTTTGTCTGCTCAAGCTTTCATTCGACATTCCTGAGGTCCTTGAGAA 87
QY 71 CAGTCCCGCT 130
DB 88 TCGTCT 147
QY 131 GCGTGTATATCTCTGATAGGCTCTCACTGCTGCTGATATCCCATGATCTTTTCCC 190
DB 148 CTCATAGCCCTTCTGCTGATGACATCTCTGACATCTCTGACACCCCATGATCTTTTCTG 207
QY 191 TTAACTTGTCT 250
DB 208 GCCAATCT 267
QY 251 AGTTTGTCTCAAGAAACATTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 310
DB 268 AGCTTGTGTAGAGCCAGAGAGATCTCTAGGAGAGATGAGCCACAGATGTTTTC 327
QY 311 TTCTGTTTCT 370
DB 328 TTCACTTTTCT 387
QY 371 GTGGGATCTGTAAACCACTGTTGTACAGATCAACCATGCTCCAGGCTGTCTGCTC 430
DB 388 ATGGGCAATATGCTCCCACTCTATGCAACCCGATAGTGTAGATATGTCCTTCC 447
QY 431 CTTTACTGGGTCTACAGGATGGGGGTTTGTGGGCTGTGCTCATACAGAAATATA 490
DB 448 TTGGCAATTTTTCATGGGAAATGGGATGATGATGATGATGATGATGATGATGAT 507
QY 491 GTGTTTCTACCTTTTGTGAGACAACTTGTCAATCACTAGTGTGATCTTCC 550
DB 508 TNCCTTGAACCTTGTGAGACCTTGTGAGATAGACCACTTCTTCTGTGACCTTCCACT 567
QY 551 CTTTCTAGCTCTCTCTCAACGCTCTTACATAAATGCTGTGATCTTTATTTTGTG 610
DB 568 CTCCTGCACTGTGCTGTGAGATATACATCCAAAGAGGCTGCCATCTTTGTGGCAGCA 627
QY 611 ACCGTGGCATTTGGGGGCCCATTTGTCGCTTTTATCTCTATAGTTTATCTTTC 670

DB 628 ATCTCTGATATATAGTCCATTTTGTGATCTTTATTTATATGCAATTTCTGTT 687
QY 671 AGCATTCCTCCGCTTATGTTCTGTGAGGACAGTCTTAAACCTTCACTGATGCTCC 730
DB 688 GCAGTCTGTGATGCTTCTTACTGAGGCGGCATTAAGCTCTTCCACTGTTCTCA 747
QY 731 TACATATGACATTTCTCTTTCTTTTGGGTGAGAGCTTTTACGTAACCTCAACCCCT 790
DB 748 CACCTACTGTATGACACCTTTTATGCTGTGTCCTTTTACCTATTTGAGGCCAAG 807
QY 791 TCCATTTTACCCTGACAGGAGGAAAGTCTCCCTGTTCTTATACCACTGTGTGCCC 850
DB 808 TCTAGCCACTACAGAAATGACAAACTTGGCCCTCTTACACAGAGATGACATCC 867
QY 851 ATGTTTAACTTATATCTACAGCTGAGAAATAGATGTCAACTTGCCTGGAAGCA 910
DB 868 ATGCTGAACCTTATCTACCTTACGCTTACAGAACAGAAAGTCAAGGACGACAGAGA 927
QY 911 ACCTTTCCAGAAATAGCTTTCTTGAAAAA 942
DB 928 ACTCTGACCTGAAAAAATTAATGCAATTAA 959

RESULT 15
US-09-016-434-1056
Sequence 1056, Application US/09016434
Patent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1056:
SEQUENCE CHARACTERISTICS:
LENGTH: 1990 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 91041044
US-09-016-434-1056

Query Match 21.5%; Score 206.8; DB 4; Length 1990;

Best Local Similarity 51.8%; Pred. No. 1.4e-54;
Matches 469; Conservative 0; Mismatches 437; Indels 0; Gaps 0;

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QY      4 GGCCTGCCGAACTCCCTCCGTGACAGAGTTTATCCCTGCAGGCTTATCCACCACC 63
Db      496 GGCATGATATCAAAAGCTCCACACCGGGCTTCCCTCTCGGCTTCTGAAACACC 555
QY      64 GGGACTCCAGGCTCCCGTCTTCTCTGTTTCTAGTTTCTACGGGCTACGGTGGTGG 123
Db      556 AAGGCTGGAGAGACTCTTCTGATGATCACTTCTCACTCCCTAACCTAGTGGG 615
QY      124 GAACCTGGGCTTGATATCTGATAGGCTCACTCGCTGCATATCCCATGTACTT 183
Db      616 CAACACATCATCATCTGCTGTCTGCGCTGACACCAAGCTCCACTCTCCATGTACTT 675
QY      184 TTTCCTCTCAACTGTTCCCTCTGTAGATTATGTTTCTTACAGACATCATTCGAAAT 243
Db      676 TTTCCTCTCAACTCTCTCTCTGACCTCTGTTTCAACAGAGTTGTGCCCAAT 735
QY      244 GCTGATGAGTTTGTCTCAAGGAGACATTAATTCCTTCAAGGCTGTATGATCACTT 303
Db      736 GCTGACCACACTCTGGGGCCCAAGACATCACTTCTGAGCTGTCTGTCCAGAT 795
QY      304 CTTCTTCTTCTGTTCTTCTTCTTCTTCTGAGTCTTCAATCCTGTGCGAGTGTGAGA 363
Db      796 CTTCACTTCTCTGCTCCCTGGGACACATGAGTCACTCTCATGAAGATGCTTTGA 855
QY      364 CCGCTAGCTGGGACATCTGTAAACCACTGTGTACACGATCACTGCTCCCAAGTGTG 423
Db      856 TCGCTAGCTGTGTCTGCAAGCCCTCTCACTATGCCACATCCACCCCGCTGTG 915
QY      424 TTGCTCTTTTACTGTGCTGTCTAAGGATGGGGATTTTGGGCTGTGCTCATACAGG 483
Db      916 CTGGAGCTGGCATCTGTGGCTGGGTCTATGGGTAGTGGGTCAATGATCCAGACACC 975
QY      484 AATATATGTTTCTGACCTTTTGTGCAAGACACTTGTCAATCACTACATGTGTACAT 543
Db      976 ATCCACCTGCACCTGCCCTTCTGCCCGATCGGACAGTGTGATTTGTCTGTAGGT 1035
QY      544 CTTTCCCTCTTGAAGCTCTCTGCAAGGCTTTACATAAATGTCCTGATCTTTAT 603
Db      1036 CCGAGCTATATGTGACCTCTCTGTGAAGACCTCTCAATATGATCCAGTGGCTGT 1095
QY      604 TGTGTGACCGTGGCATGGGGTGGCCATGTGTGCCGTTTATATCTTATGTTTAT 663
Db      1096 TGCAGGTCTTCACTTGTGTGTGCTCTGAGCTCATCTGTCTTACGAGGCAT 1155
QY      664 TCTTTCAGCATTCCTCGCGTTAGTTCTGCTGAGGAGGAGGTCTAAAGCTTCACTG 723
Db      1156 TACCTGGGCACTGCTGAGGATTAATCCGCAAGCATGAGAGAAAGGCTTTGGACCTG 1215
QY      724 CAGCTCTCAATAATGCAATTTCTCTTTCTTGGGTCAAGAGCTTTTACGTACCTCA 783
Db      1216 CTCTCCCATCTCACTGTGTGACACCTCTTCTACAGCTCATGTGCTGTACCTCCA 1275
QY      784 ACCGCTTTCATTTTACCCCTGACACAGGAGAAAGTCTCTCCCTGTCTATACACTGT 843
Db      1276 GCCCAAAATCCGATATGCCCAAGGAGGAGGAGGCTTTGTGTCTTCTATGCACTGG 1335
QY      844 GGTGCCCATGTTTATACCATTAATCTACAGCTGAGGATATAGATGTCAAATTCCT 903
Db      1336 CACTCTTCACTTACCTCTCTGTATACCTCTGAGAACAGAGATTAAGCGACACT 1395
QY      904 GAAGAG 909
Db      1396 CAGGAG 1401
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Search completed: September 30, 2004, 01:24:09
Job time : 95 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 29, 2004, 22:53:21; Search time 3085 Seconds
(without alignments) 9321.647 Million cell updates/sec

Title: US-10-023-597-23

Perfect score: 963
Sequence: 1 ataggctgcgcagaaactcctcctt.....ttttagaacaagaaagaga 963

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database:

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2: em_esthum:*
3: em_estin:*
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13: gb_est4:*
14: gb_est5:*
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26: em_gss_phg:*
27: em_gss_vit:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	691.6	71.8	933	29	AY407109 Homo sapi
2	623	64.7	903	29	AY405609 Homo sapi
3	602.8	62.6	933	29	AY407111 Mus muscu
4	580.6	60.3	799	29	AY407110 Pan trogl

Result No.	Score	Query Match	Length	DB ID	Description
5	556.8	57.8	899	29	AY405610 Pan trogl
6	547.8	56.9	903	29	AY405611 Mus muscu
7	456.6	45.3	930	29	AY405657 Homo sapi
8	427	44.3	930	29	AY405659 Mus muscu
9	394.8	41.0	930	29	AY419056 Pan trogl
10	391.8	40.7	930	29	AY419055 Homo sapi
11	388.6	40.4	930	29	AY419057 Mus muscu
12	358.6	37.2	625	29	CE158635 tigr-gss-
13	350.6	36.4	625	29	CE158635 tigr-gss-
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15	333.2	34.6	726	28	AZ255734 RPT-23-1
16	312	32.4	848	28	BZ281255 CH230-344
17	309.6	32.1	636	14	CB174480 OR_20E1H1
18	307.2	31.9	472	14	AO503914 RPT-11-2
19	303.2	31.5	472	14	CA880338 KO982C03-
20	302.8	31.4	626	29	CE184619 tigr-gss-
21	302.6	31.4	617	14	CB174340 OR_2042A0
22	300.6	31.2	616	28	CB174340 OR_2042A0
23	299	31.0	733	28	BH342053 CH230-303
24	297.8	30.9	664	14	CB173618 OR_2021B1
25	290.6	30.2	933	29	AY405612 Mus muscu
26	286.2	29.7	444	14	CA881328 KO982C03-
27	286.6	28.0	475	28	AZ016145 RPT-23-3
28	268.6	27.6	731	28	BZ207385 CH230-487
29	266.2	27.6	752	28	BZ102526 CH230-238
30	265.4	27.6	942	29	AY402814 Pan trogl
31	263.4	27.4	942	29	AY402813 Homo sapi
32	262.6	27.3	634	10	BB635510 BB635510
33	260.6	27.1	945	29	AY402815 Mus muscu
34	255	26.5	650	14	CB174356 OR_2041F0
35	254.4	26.4	945	29	AY404155 Mus muscu
36	254.2	26.4	945	29	AY415715 Mus muscu
37	250.2	26.0	649	28	BH342817 CH230-64F
38	248	25.8	936	29	AY405001 Pan trogl
39	246.2	25.6	936	29	AY405001 Pan trogl
40	245.6	25.3	547	14	CB173631 OR_2021H0
41	243.6	25.3	897	29	AY405605 Mus muscu
42	243	25.2	631	10	BB201968 BB201968
43	241.4	25.1	654	14	CB174038 OR_2032D0
44	240.8	25.0	900	29	AY401567 Mus muscu
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ALIGNMENTS

RESULT 1
AY407109 933 bp DNA linear GSS 15-DEC-2003
DEFINITION Homo sapiens ORB12 gene, VIRTUAL TRANSCRIPT, partial sequence.
LOCUS AY407109.1 GI:39763080
ACCESSION AY407109
VERSION AY407109.1
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
Direct Submission

JOURNAL

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES

source

Location/Qualifiers

1..933

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

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/gene="OR8B12"

/locus_tag="HCW2781"

ORIGIN

Query Match 71.8%; Score 691.6; DB 29; Length 933;
Best Local Similarity 84.0%; Pred. No. 2e-154;
Matches 781; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

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DB      4 GAGCCAAAACCTCTCTGTGACAGATTATCTTCGACAGGCTTAAACCCACCGCGGA 63
QY      68 CTCAGATCCCGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 127
DB      64 CTGCGGATCCCGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 123
QY      128 CTGGGCTTGATATCTCTGATAGGGCTCAACTCTGCGCTGCAATCCCATGACTTTTTC 187
DB      124 CTGGGCTTGATAACTCTGATAGGGCTCAACTCTGCGCTGCAATCCCATGACTTTTTC 183
QY      188 CCCTTCAACTGTCCCTGATGATTTTATGTTTCTCTACAGCATCATCTCCCAAAATCTG 247
DB      184 CTTTAACTCTCTTAAATGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 243
QY      248 ATGAGTTTGTCTCAAGAAACATTTATCTCTCAAGGCTATGATGACTTCTTC 307
DB      244 ATGAGTTTGTCTCAAGAAACATTTCTCTCTCAAGGCTATGATGACTCTCTTC 303
QY      308 TTCTTCTGTTCTTGTCTTCTGAGTCCTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 367
DB      304 TTCTTCTGTTCTTGTCTTCTGAGTCCTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 363
QY      368 TACGTGGCATCTGTAACCACTGTTTACAGTACACATGTCCTCCAGGCTGTTTG 427
DB      364 TACGTGGCATCTGTAACCACTGTTTACAGTACACATGTCCTCCAGGCTGTTTG 423
QY      428 CTCTTTTACTGAGTGTCTACAGGATGGGGTCTTTTGGGGTGTGGCTCAATACAGAAAT 487
DB      424 CTCTTTTGTGGGCTATGGGATGGGGTCTTTTGGGGTGTGGCTCAATACAGAAAT 483
QY      488 ATAGTGTCTACACTTTTGTGACAGAACCTTGTCAATCACTACATGATGATCTT 547
DB      484 ATAGTGTCTACACTTTTGTGACAGAACCTTGTCAATCACTACATGATGATCTT 543
QY      548 CCCCTTTTGAAGTCTCTCTGACAGGCTCTTACATAATGTCTGTGATCTTTATTTT 607
DB      544 CCCCTTTTGAAGTCTCTCTGACAGGCTCTTACATAATGTCTGTGATCTTTATTTT 603
QY      608 GTGACGCTGTCATGGGGTCCCATGTTGCGGTTTATNCTTAAATGTTTATTTT 667
DB      604 GTGACGCTGTCATGGGGTCCCATGTTGCGGTTTATNCTTAAATGTTTATTTT 663
QY      668 TCCAGCATTTCCCGCTTAACTGCTGAGGGGAGGTCTAAAGCTTCACTAGCTCAG 727
DB      664 TCCAGCATTTCCCGCTTAACTGCTGAGGGGAGGTCTAAAGCTTCACTAGCTCAG 723
QY      728 TCCAGCATTTAGAGTTCTCTTTCTTGGGTCAGGAGCTTTTACATGATCTCAACCC 787
DB      724 TCCAGCATTTAGAGTTCTCTTTCTTGGGTCAGGAGCTTTTACATGATCTCAACCC 783
QY      788 CTTTCAATTTTACCCCTGACACAGGGGAAAGTCTCTCTCTTCAATACATGATG 847
DB      784 CTTTCAATTTTACCCCTGACACAGGGGAAAGTCTCTCTCTTCAATACATGATG 843

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QY      848 OCCATGTTTAAACCATTAATCTACAGCTGAGGAAATAGATGTCAACTGCGCTGAAG 907
DB      844 CCGTGTTAAACCATTAATCTACAGCTGAGGAAATAGATGTCAACTGCGCTGAAG 903
QY      908 AGAAGCTTTTCAGAAATTAAGCTTTTCTGA 937
DB      904 AGAAGCTTTTCAGAAATTAAGCTTTTCTGA 933

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RESULT 2

AY405609

LOCUS

DEFINITION

Homo sapiens OR8B8 gene, VIRTUAL TRANSCRIPT, partial sequence.

AY405609

ACCESSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

gene

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

<1..>903

/gene="OR8B8"

/locus_tag="HCW281"

ORIGIN

Query Match 64.7%; Score 623; DB 29; Length 903;
Best Local Similarity 80.6%; Pred. No. 4.9e-138;
Matches 728; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

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QY      35 TTATCTCTGAGGTTTATCCACGCGGAGCTCCAGGCTCCGCTCTCTCTCTCT 94
DB      1 TTATCTCTGAGGTTTATCCACGCGGAGCTCCAGGCTCCGCTCTCTCTCTCT 60
QY      95 CTAGGTTTCAACGCGGTCAAGGCTGAGGAACTGGGCTTGATTAATCTGATAGGCTC 154
DB      61 CTAGGTTTCAACGCGGTCAAGGCTGAGGAACTGGGCTTGATTAATCTGATAGGCTC 120
QY      155 AACTGCGCTGCAATATCCCATGATCTTTTCCCTTCACTGTCCTCGTATGATTTT 214
DB      121 AACTGCGCTGCAATATCCCATGATCTTTTCCCTTCACTGTCCTCGTATGATTTT 180
QY      215 AGTTCTCTACAGACATCATTCCTCAAAATGCTGATGATTTTGTCTCAAGAAACAT 274
DB      181 TGTATTTCAAGTTTATCATCTCCCAAAATGCTGATGATTTTGTCTCAAGAAACAT 240
QY      275 ATTCTTCAAGGCTGATGATGATCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTGAG 334

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Db	241	ATCTCTCAACGAGGGGTGTAATGACTCAGCTCTTCTTCTTCTTCTTCTTCTGTCCTGAG	300
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Db	301	TCCTTCATCCCTGTGACGATAGGCGTACGACCGCATATGAGCCATCTGTAAACCACTGTG	360
OY	395	TACACGATACCATATGCTCTCCACAGTGTGTGTGCTCTTCTTACTGGGTGTCTACGGGATG	454
Db	361	TACATGTGCACCAATGTCTCCCAAGGTGTGTTTCTCTTCTTGTGTGGGTGTCTAGGGATG	420
OY	455	GGGGTTTGTGGGGCTGTGGCTCTAATACAGAAATATAGTGTTCACCTTTTGTGCAAC	514
Db	421	GGGGTTGTGGGGCGCATGGCCCAACACAGCTGACATGAGGGGTGTGACCTTGTGCCCAT	480
OY	515	AACCTTGTGCATCACTACATATGATGACATCCCTCCCTCTTGTGAGCTCTCCGAAACGC	574
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OY	575	TCTTACATTAATGTCTCTGTCATCTTTATGTGTGACCGTGTGGCATTTGGGGCCCAT	634
Db	541	ACCTATGTGATGATGAGCTTGTAGTGTGTGTGTGTGGGCATGTATATGTGTGCCACA	600
OY	635	GTTGCCGTTTATCTCTATATGTTTATCTTCTTTCACAGATCTCCGGGTAGTTCTGCT	694
Db	601	GTACCATCTTCATTTTCTATGTCTCTATCTCTTCACACATCTTCACATTTGATTTCCAG	660
OY	695	GAGGGCAGGTCTAAAGCCCTTCAGTAGCTGACAGCTCTCAATATTTGACAGTTCTCTTTTC	754
Db	661	GAGGGCAGGTCCAAAGCCCTTCGACAGCTGACAGCTCCACATATTTGACAGTTCTCTGTTC	720
OY	755	TTTGGGTAGAGAGCTTTTACGTACTCTAAACCCCTTCATTTTACCTTCCCTGACCAAGGG	814
Db	721	TTTGGGTAGAGAGCATATATGATCTCAAAACCTTTCTCTTATGATATGACCAAGGGC	780
OY	815	AAAGTCTCTCCCTGTTCTATACACTGTGTGGCCATGTTTAAACCATTAATCTACAGC	874
Db	781	AAAGTCTCTCCCTATTTCTATACACTGTGTGGGCCCATGCTCAACCATTAATTAATAGC	840
OY	875	CTGAGGAATTAAGAGATGTCAACTTGCCCTGAAAGAGAACCTTTTCCAGATAATAGCTTTCT	934
Db	841	CTGAGGAATTAAGAGAGCTCAAGTGTCTCTTAAAGAAATCTTGAAACAAATATGCAATTCCTC	900
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Db	901	TGA 903	
RESULT 3			
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LOCUS Mus musculus OR8812 gene, VIRTUAL TRANSCRIPT, partial sequence,			
DEFINITION Mus musculus OR8812 gene, VIRTUAL TRANSCRIPT, partial sequence,			
ACCESSION AY407111			
VERSION AY407111.1 GI:39763082			
KEYWORDS GSS.			
SOURCE Mus musculus (house mouse)			
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE 1 (bases 1 to 933)			
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,			
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,			
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smirsky,J.J.,			
Adams,M.D. and Cargill,M.			
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous			
gene tios			
JOURNAL Science 302 (5652), 1960-1963 (2003)			
PUBMED 14671302			
REFERENCE 2 (bases 1 to 933)			
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,			
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,			
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smirsky,J.J.,			
Adams,M.D. and Cargill,M.			

TITLE		Direct Submission	
JOURNAL		Submitted (16-NOV-2003) Celera Genomics/45 West Gude Drive, Rockville, MD 20850, USA	
COMMENT		This sequence was made by sequencing genomic exons and ordering them based on alignment.	
FEATURES		Location/Qualifiers	
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gene		/organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" <1..>933 /gene="NRB12" /locus_tag="HCM2781"	
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Best Local Similarity	78.5%	Pred. No. 3.3e-133;	
Matches	721;	Conservative 0;	Mismatches 197; Indels 0; Gaps 0
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Db	16	TCCCTGTGAATAGATTATCCTCGCAGGCGCTGACAGACCAACGAGACTCCGATGCC	75
Db	80	GCTCTCTTCCTGTTTCTAGATTCTTCAACCGGCTCACGGTGTGGGAGAACTGGGCTTGATA	139
Db	76	CTCTCTCTCTCTGTTCTTCAAGTTTCTCAACAGTGAAGTGTGGTGGAACTGGGCTTGATG	135
Db	140	ATCTGATAGGGCTCACTCTGCGCTGAAATCCCATGACTTTTCCCTTCAACTTG	199
Db	136	TCCCGATAGGGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT	195
Db	200	TCCCTCCGATTTTATGTTCTTCTCAACGACATCATTCACCAAGCTGATGATTTGTC	259
Db	196	TCTGATATGATTTCTGTTATTTCTTCCATCATCCCAAAATGCTTATGATTTTATC	255
Db	260	TCAAGAGAAACATTAATTTCTTTCACAGGGTGTATAGTCACTTCTTCTTCTGTTTC	319
Db	256	TCAAGAGAAACATCATCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT	315
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Db	440	GGTGTCTAAGGAGTGGGGGTTTGGGGCTGTGGCTCATACGAAATATAGTGTTC	499
Db	436	GGAGTCATATGATAGGCTTCTCTGGGGCATGGGCGCAATACGAGGAACCTCATGATCTG	495
Db	500	ACCTTTTGTGACAGAACCTTGTGATCATCATCATCATCATCATCATCATCATCATCATCAT	559
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Db	560	CTCTCTGTGACAGGCTTGTATCAATATGTCTGTGATCTTATTTGTTGTGAACCGTTGC	619
Db	556	CTCTCTGTGACAGGCTTGTATCAATATGTCTGTGATCTTATTTGTTGTGAACCGTTGC	615
Db	620	ATTGGGATGCCATTTGTTCCGCTTTTATCTGTAAAGTTTATCTTCCAGCATCTC	679
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Db	680	CGGCTTAGTCTGTGCTGAGGGAGGCTTAAAGCTTCAATAGTGCAGCTCTCAATATAT	739
Db	676	CCCATGATTCACAGAGGGAGGCTTCAAGGCTTCAAGACCTGACGCTCCCATCTGAT	735
Db	740	GCAGTTTCTTTTCTTTTGGCTCAGAGCTTTTATGATCTTAAACCCCTCCATTTTA	799
Db	736	GTGGTTTCTTTTCTTTTGGCTCAGAGCTTTTATGATCTTAAACCCCTCCATTTT	795
Db	800	CCCTGACACAGGGGAAATGTCCTCCCTCTATATACCTGTGTGCTCCATGTTTAC	859

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Db 856 CCTCGATCTATAGCTGTGAAATATAGATGTCMAAGTTGCTCTAGAGAAACTTTGGT 915
QY 920 AGAATAAGCTTTTCTTGA 937
Db 916 AAGAGAAATCTTCTTAA 933

RESULT 4
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LOCUS Pan troglodytes OR8B12 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY407110
VERSION AY407110.1 GI:39763081
KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee).
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1 (bases 1 to 799)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanendbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Interfing nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302

2 (bases 1 to 799)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanendbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source location/Qualifiers
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Best Local Similarity 83.0%; Pred. No. 6.5e-128;
Matches 661; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

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Db 4 GCAGCAAAACTCTTGTGACAGAGTTATCTCGAAGCTTAAACCAAGCCGGA 63
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Db 64 CTGGGAGATCCCTCTTCTTCTTCTTCTGTTCTGAGTTTCAATGTCACCGTGGGGAAC 123
QY 128 CTGGGCTGATATCTGATAGAGGCTCACTCGCTGATATCCCAATGTTCTTTT 187
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QY 188 CCTTCAACTTGTCTCTGATGATTTAGTTTCTCTGACACATCATTTCCAAATGCTG 247
Db 184 CTTTAACTCTCTTTAAACAGATTTCGTTTCTCCAGTACCATCTCCCAAAATGCTG 243
QY 248 ATGAGTTTGTCTCAAGGAAGACATATTTCTTCAAGGAGTGTATGAGTCAAGTTCTTG 307

Db 244 ATGAGTTTGTCTCAAGGAAGACATATTTCTTCAAGGAGTGTATGAGTCAAGTTCTTG 303
QY 308 TTTCTCTGTTCTTTTGTCTTTTCTGAGTCTTCTTCTGAGTCTTCTGAGGAGAGAGCCG 367
Db 304 TTTCTCTGTTCTTTTGTCTTTTCTGAGTCTTCTTCTGAGTCTTCTGAGGAGAGAGCCG 363
QY 368 TACGAGGATCTGTAACCACTGTTGTAACAGATATCATGATCTTCCAGGAGTGTG 427
Db 364 TATGAGGATCTGTAACCACTGTTGTAACAGATATCATGATCTTCCAGGAGTGTG 423
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QY 488 ATAGTGTCTTCACTTTTGTGAGACAACTTGTCAATCATATGATGATGATCTT 547
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Db 784 CTTNCAATCTGCCCC 799

RESULT 5
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LOCUS Pan troglodytes OR8B8 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY405610
VERSION AY405610.1 GI:39761584
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1 (bases 1 to 899)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanendbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Interfing nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302

2 (bases 1 to 899)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanendbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source location/Qualifiers
1..899

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Best Local Similarity 73.1%; Pred. No. 3,2e-122;
Matches 657; Conservative 0; Mismatches 242; Indels 0; Gaps 0;

QY 35 TTATCTCGAGGCTTAAATCCACGCGGAGCTCCAGTCCCGCTCTTCTCTGTT 94
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QY 95 CTAGCTTTCTAGCGGCTCAAGTGTGGGGAACCTGGGCTTGAATCTCTATAGGCTC 154
DB 61 CTAGGCTTCTAGCTGTCTAGTGTGGGGAACCTGGNNNNNNNNAACNNGTAAAGTCTC 120
QY 155 AACTCGCGCTGCAATATCCCAATGTAATTTTCCCTCACTTGCCCTCGATATTT 214
DB 121 AACNNTCAGNNACACCCCTNNNNNACNTCTCTCTATACCTTGCTTCAATATTC 180
QY 215 AGTTTCTAGACGACATCATTTCCAAATGCTGATGATGTTTGTCTCAAGAAACATT 274
DB 181 TGTATTTCCANNNTTATCACTCCCAAAATGCTGATGCTTGTCTTANNNNNNACGC 240
QY 275 ATTCTCTGACAGGGGTATGATGATGCTCTTCTTCTGTTCTGTTCTTTCTGAG 334
DB 241 ATCTCTAGGAGGANNNTATGACTCANNNTCTTCTTCTTCTTCTTGTCTCTGAG 300
QY 335 TCCTTCATCTCTGTGGCGATGTGTGAGAGACCGCTACGTGGGACATCTGAACCACTTTG 394
DB 301 TCCTTCATCTCTGTGGCGATGTGTGAGAGACCGCTACGTGGGACATCTGAACCACTTTG 360
QY 395 TACAGCATCAGCATGTCTCCCGAGGTGTGTCTCTTCTTCTGAGGTGTCTACGGGATG 454
DB 361 TACATGTATGACCAATGNNCCCGAGGTGTGTCTCTTGTGTGGNNNNNATGGGAGT 420
QY 455 GGGGTTTTGGGCTGTGGCTATACAGAAATATATGTTTCTACCTTTTGTGAGAC 514
DB 421 GGGTGTGGCTGTGGCTATACAGAAATATATGTTTCTACCTTTTGTGAGAC 480
QY 515 AACCTGTCAATACATGATGTGACATCTTCCCTTCTTGAAGCTCTCTGCAAGGC 574
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QY 635 GTTGGCTTTTATCTTATGATTTTATTTCTTCCAGCATCTCTCGGATGATTTGCT 694
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DB 661 GAGGCGAGCTTAAAGCTTCACTAGTGTGAGCTCTATATATTCAGATTTCTTTTC 720
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DB 841 CTGAGAAATAGAGTGTCAAACTGCGCTGAAGAAACCTTTTCCAGAAATTAAGCTTTTC 899

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RESULT 6
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LOCUS
DEFINITION
Mus musculus OR8B8 gene, VIRUAL TRANSCRIPT, partial sequence,
ACCESSION
AY405611
VERSION
AY405611.1 GI:39761585
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORANISM
Mus musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 903)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,
Adams,M.D. and Cargill,K.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios.
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 903)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,
Adams,M.D. and Cargill,K.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
location/Qualifiers
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Query Match      56.9%; Score 547.8; DB 29; Length 903;
Best Local Similarity 75.4%; Pred. No. 4.5e-110;
Matches 681; Conservative 0; Mismatches 222; Indels 0; Gaps 0;

QY 35 TTATCTCGAGGCTTAAATCCACGCGGAGCTCCAGTCCCGCTCTTCTCTGTT 94
DB 1 TTTATCTCGAGGCTTAAATCCACGCGGAGCTCCAGTCCCGCTCTTCTCTGTT 60
QY 95 CTAGCTTTCTAGCGGCTCAAGTGTGGGGAACCTGGGCTTGAATCTCTATAGGCTC 154
DB 61 CTAGTGTCTAGCGGCTCAAGTGTGGGGAACCTGGGCTTGAATCTCTATAGGCTC 120
QY 155 AACTCGCGCTGCAATATCCCAATGTAATTTTCCCTCACTTGCCCTCGATATTT 214
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QY 215 AGTTTCTAGACGACATCATTTCCAAATGCTGATGATGTTTGTCTCAAGAAACATT 274
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DB 301 TCTTTATCTGTGACGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
QY 395 TACAGCATCAGCATGTCTCCCGAGGTGTGTGTCTCTTCTTCTTCTTCTTCTTCTTCT 454
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QY 455 GGGGTTTTGGGGCTGGGCTCATACAGGAATATATGTTCTGACCTTTTGGACAG 514
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 DB 481 AACATGTTCACACATATATGTGTATCTTCCCTTCTTGGAGACATCCGTATACAGC 540
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 QY 635 GTTCCGCTTTTATCTTATGATGTTTATTTTCTTCCAGATCTCCGGTAGTCTCT 694
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 QY 695 GAGGCGAGGCTTAAAGCTTCAAGTGTGACGCTCTTCAATATTCAGATTCTCTTTTC 754
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 QY 755 TTTGGGTGAGAGCTTTTACGTAAGCTCAAAACCCCTTCATTTTACCCCTGAGACAGGG 814
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 QY 815 AAGTGTCTCTCTCTTCTTATACCACTGTGTGCTTAAACCATTAATCTACAGC 874
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 QY 935 TGA 937
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RESULT 7
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 LOCUS Homo sapiens OR8B4 gene, VIRUAL, TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 AY405657
 ACCESSION AY405657.1 GI:35761631
 VERSION GSS.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 930)
 AUTHORS Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Ciovello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trics
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 930)
 AUTHORS Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Ciovello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
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RESULT 8
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DEFINITION
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AY405659
ACCESSION
AY405659
VERSION
AY405659.1
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 930)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
JOURNAL
PUBMED
2 (bases 1 to 930)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
COMMENT
TITLE
JOURNAL
AUTHORS
FEATURES
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Matches 623; Conservative 0; Mismatches 305; Indels 3; Gaps 1;
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DB 1 ATGGCTGCCGAGAACTCTCTCGAGAGAGTTATCTCTGGAGATTTTCAACGCA 60
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QY 122 GGGAACTCGGCTTGATATCTCGATAGGCTCACTCTCGCTGATATCCCAATGAC 181
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QY 662 ATCTTTCAGCATCTCTCCGTTAGTTGTCTGAGGCAAGGTTAAAGCTTCAGTAC 721
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QY 782 AAACCCCTCTCATTTTACCCTGAGACAGGGAAGTGTCTCTCTCTTCTATACCACT 841
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RESULT 9
AY419056
LOCUS
DEFINITION
Pan troglodytes OR8A1 gene, VIRTUAL TRANSCRIPT, partial sequence,
AY419056
ACCESSION
AY419056.1
VERSION
AY419056.1
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
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1 (bases 1 to 930)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
JOURNAL
PUBMED
2 (bases 1 to 930)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
These sequences were made by sequencing genomic exons and ordering
them based on alignment.
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JOURNAL
AUTHORS
FEATURES
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DB 61 GGAGAGCTTCAGCTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 122 GGAAGCTGGGCTGATATCTCTGATAGGCTCACTCTCGGCTGCAATATCCCATGTAC 181
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DEFINITION Homo sapiens OR8A1 gene, VIRTUAL TRANSCRIPT, partial sequence.

ACCESSION AY419055 genomic survey sequence.

VERSION AY419055.1 GI:39775015

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 930)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,

Perriere, S., Wang, G., Zheng, X.H., White, T.D., Shinsky, J.D.,

Adams, M.D. and Cargill, M.

Direct Submission

Rockville, MD 20850, USA

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

These sequences were made by sequencing genomic exons and ordering

chem based on alignment.

Location/Qualifiers

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source

COMMENT

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chem based on alignment.

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Qy 722 TGACGCTCTACATAATATGCAATTTCTCTTTCTTTGGGTGAGAGCTTTACGTACTTC 781

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Db 898 GTGCAGAAACGCTGAGGGGTAACTGTGTTT 928

RESULT 11	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	
AY419057		Mus musculus Oribal gene, partial sequence, genomic survey sequence.	AY419057	AY419057.1	GI:39775017	GSS.	Mus musculus (house mouse)	Elkayova; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,D.J., Adams,M.D. and Cargill,M.	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios	Science 302 (5652), 1960-1963 (2003)	14671302	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,D.J., Adams,M.D. and Cargill,M.	Direct Submission	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	These sequences were made by sequencing genomic exons and ordering them based on alignment.	Location/Qualifiers	1..930	/organism="Mus musculus"

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625 bp DNA linear GSS 25-SEP-2003

CE158635
VERSION
KEYWORDS
SOURCE

CE158635.1 GI:35286025
GSS.
Canis familiaris (dog)

ORGANISM
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REFERENCE
1 (bases 1 to 625)
Kirkness, E.F., Balna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.

THE dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)

JOURNAL
MEDLINE
PUBMED

22875432
14512627

COMMENT
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org

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Classes: Shotgun.

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Best Local Similarity 80.2%; Pred. No. 6.9e-75;
Matches 421; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

20 TCCTCCGTGACAGAGTTATCTCGACAGCTTAATCCACGCGGAGCTCCAGTCCCC 79
101 TCCTCTGACAGAGTTATCTCTCAGAGCTTAACCAACGAGACTCCAGATTCTT 160
80 GTCT 139
161 CT 220
140 ATCTGATAGAGGCTCACTCTCGAGTGAATCCCATGATCTTTTCCCTCAACTG 199
221 ACCCTGATGGGCTCAATCTTCACTGCAACCCCATGATCTTTTCTTCAACTG 280
200 TCCTCTGATAGTTAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 259
281 TCCTCTGATAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 340
260 TCAAGAGAGACATATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 319
341 TTGAGAGAGAGATCT 400
320 TTTGCT 379
401 TTTGCT 460
380 TGTAACTGATCT 439
461 TGTAACTGATCT 520

Qy 440 GGTGTCTACGGAGTGGGGGTTTTTGGGGCTGTGGCTCATACAGAAATATAGTTTCTC 499
Db 521 GGTGTCTATGTATGGGGTTTGGCTGAGGCATGGCCACAGTGTGATGTAAGACTG 580
Qy 500 ACCCTTTGTGACAAACCTTGTCTCATCTACTATATGTGACATC 544
Db 581 ACCCTTGTGACAAACCTTGTGACATCTACTATATGTGACATC 625

RESULT 13
CB174479
LOCUS

DEFINITION OR_2052H11.020911.y1 Embryonic mouse olfactory epithelium library
Mus musculus cDNA clone 205H11 5', mRNA sequence.

748 bp mRNA linear EST 09-OCT-2003

CB174479
VERSION
KEYWORDS
SOURCE

CB174479.1 GI:37593108
EST.
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 748)
Young, J.M., Shykind, B.M., Lane, R.P., Tonnes-Priddy, L., Ross, J.A.,
Walker, M., Williams, E.M. and Trask, B.J.

Odorant receptor expressed sequence tags demonstrate olfactory
expression of over 400 genes, extensive alternate splicing and
unequal expression levels

Genome Biol. 4 (11), R71.1-R71.15 (2003)

CONTACT: Young JM
Trask Lab, Division of Human Biology
Fred Hutchinson Cancer Research Center
1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA
98105-1024 USA

Tel: 206 667 1471
Fax: 206 667 6524
Email: jayoung@fhcrc.org

Young gene new name GA_X6K02P2PVD-32156773-32157705
Young gene old name GA_X5JB760M-114653-1145421
Zhang gene name MOR167-3

Seq primer: M13 Reverse

Location/Qualifiers

1..748

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/clone="205H11"
/issue_type="Olfactory and respiratory epithelium"
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/note="Organ: Olfactory turbinates; Vector:
LambdazAPII-XR; Site 1: EcoRI; Site 2: XhoI; This library
was provided by Tyler Outforth. mRNA was prepared from the
olfactory and respiratory epithelium of mixed
Swiss-Webster and C57BL/6 embryos, aged E16.5-E18.5.
Oligo-dT primed cDNA was directionally cloned into
Stratagene's lambdazAPII-XR vector."

ORIGIN

Query Match 36.4%; Score 350.6; DB 14; Length 748;
Best Local Similarity 69.8%; Pred. No. 5.7e-73;
Matches 473; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

237 CCAAAATGCTAGTATTTGTCTCTAAGAGAGACATATTTCTCTCAAGGCTGTATGA 296
Db 1 CAAAATGCTAGTATTTGTCTCTAAGAGAGACATATTTCTCTCAAGGCTGTATGA 60
Qy 297 GTCACT 356
Db 61 CCAGCTATATTTCT 120
Qy 357 TGAAGACCGCTACGTGGGACATCTTAACCACTTTTATACAGATACACATGTCTCCCC 416

Db		121	CTTATGATCGCTATTGTGGCCATCTTTAATCCACTCTTTGACAGGTTGCCATGTCCCTTA	180
Oy		417	AGTGTTGTTTGTCTCCTTTTACTGGGTTGTCACGGGATGGGGTTTTTGGGGCTGTGGCTC	476
Db		181	AATGTGTGTTGAACCTTATGCTTGTGTACAATGCAATGGAATGGAATTTTCTGGTGCAAGGCTC	240
Oy		477	ATAAGGAATAATAGTGTTCACACCTTTTGGCAGAACACCTTGTCAATCACTACATCATGT	536
Db		241	ACACGAGTAGCAGNCTGAGACTGACCTCTGTGTATGCTTAACCACCAACCACTACTCTCT	300
Oy		537	GTCATCCTCTCCCTCTTTGAGCTCTCTCGACGAGGCTCTTACATTAATGTCTGTGTC	596
Db		301	GTGATCATCTCCTCTGTGTATGACGCTCTCTGTGACAGCACCACTATGTCAATGAGCTGTATG	360
Oy		557	TCTTATTTGTTGTATACCGTTGGCATTTGGGGTGCCTATGTTGCCGTTTTTATCTTTATG	656
Db		361	TTTTCATTTGTTGTGGGCATCAATATCATATGTCACAGATCACTATCTTCATCTCTTATG	420
Oy		657	GTTTATTTCTTTTCCAGCAATCTCCCGCTTAGTTCGTGTAGGGGAGCTCTAAAGCTTCA	716
Db		421	GCTTATCTCTCTCCAGCAATTTTTCACATCAATGCAATGAAGAAGGAGCTTCAAGGCTTCA	480
Oy		717	GTAGCTGACGCTCTCAATATATGTCAGTTTCTCTTTCTTTGGTGTACGAGCTTTTACGT	776
Db		481	GCACCTGCAAGTCCACATTAATGACAGTTGTCTCTTTTGGATCAGGTGCATTTATGT	540
Oy		777	ACCTGAACCCCCCTTCAATTTTACCCCCTGGACACAGGGGAAGTGCTCCCTCGTTCTATA	836
Db		541	ATCTTAACCATCTTCTCTTCTATCTATGATCAAGGAAACCTCTCTGTGTTTTATA	600
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Oy		897	TTGCCCTGAAGAACT 914	
Db		661	TAGCCCTGAAAAACCT 678	
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LOCUS				GSS 26-JUL-2000
DEFINITION		RPCL-23-16619..TJ RPCL-23 Mus musculus genomic clone RPCL-23-16619,		
ACCESSION		RPCL-23-16619		
VERSION		AZ255734		
KEYWORDS		AZ255734.1 GI:9458784		
SOURCE		GSS:		
ORGANISM		Mus musculus (house mouse)		
REFERENCE		Mus musculus		
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus. 1 (bases 1 to 726) Zhao,S., Nierman,W., Feidblum,T., Malek,J., Shatsman,S., Akhter,B., Levins,M., McGann,S., Tsegeye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.		
TITLE		Mouse BAC End Sequences from Library RPCL-23		
JOURNAL		Unpublished (1999)		
COMMENT		Other GSSs: RPCL-23-16619.TV Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhao@ligr.org Clones are derived from the mouse BAC library RPCL-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BAC/RAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.ligr.org/cdb/bac.ends/mouse/bac_end_intro.html Plate: 166 row: I column: 9		

FEATURES		Seq primer: SP6
source		Class: BAC ends
Location/Qualifiers		
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/strain="C57BL/6J"		
/db_xref="taxon:10090"		
/clone="RPCI-23-16619"		
/sex="Female"		
/lab_host="DH10B"		
/clone_id="RPCI-23"		
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL life Technologies)." " "		
ORIGIN		
Query Match	36.4%; Score 350.2; DB 28; Length 726;	
Best Local Similarity	67.8%; Pred. No. 7.1e-73;	
Batches 490; Conservative	0; Mismatches 233; Indels 0; Gaps 0;	
75	TCGCCGCTTCTTCTGTTTCTAGATTCTACGGGTACGGTGGGAGACCTGGACT	134
3	TCCCTGCTTCTTCTGTTTCTGTTATGATATATGATATGATATGATACCGGGAATTTGGGT	62
135	TGATTAATCTGATAGGGCTCACTCTGCTGCAATGCCCATATCTTTTCCCTCTCA	194
63	TGTAATTTCAATGGAGCTGAATTTCACTTCAACCCGAGTACTTTTCTCTTCA	122
195	ACTGTCCCTGATGATTTTATGTTCTCTACAGCAATCATCTCCCAATATGCTGATGATT	254
123	ACTGTCTTTGATAGACCTCTGTTAGCTCTTCAAGTGTACACCCAAATGCTGTGAACT	182
255	TTGTCTCAGGAGAACATTTATTCCTTACAGGGGTGATGATGATGCTTCTTCTCTCT	314
183	TCATATTAAATAAATAATTTATCTCTTAACGGGGGTGATGACCAACTCATTTTATTT	242
315	GTTCTCTTGTCTTTCTGAGTCCTTCAATCCGTGGGGATGGTGGAGACCGCTAGCTG	374
243	CATCTTTGTTATTTCTGAGTGTATGTGTTAATGTCATATGCTATGATGCTATGATG	302
375	GCACTCTGAAACCACTGTTGTACACGATCAACCATGTCTCCCAAGGTGTTTGTCTCTT	434
303	CCATCTGTAATCCACTCTTATATATATATGCTATGACCTTAAATATGTTCTATCTTA	362
435	TACTGGGTCTACGGGATGGGGTTTTGGGGGTGGGCTGACACAGGAATATATGAT	494
363	TGCTTGGTCAATCTTATATGACATTTTCTGTGTCATAGGCTCACACAGGATGATGTTAA	422
495	TTCTCACCTTTTGTGACAGACACCTTTGATCATCTACTATGATGATGATCCTTCCCTTC	554
423	GATGACCTTCTGTGATGCAAAACCATCATCATCACTACTTCTGTGACATCTCTCTGGA	482
555	TTGAGCTTCTCTGCAAGGCTCTTACATTAATATGCTGCTCATCTTATTTGTGTACCG	614
483	TGACAGCTTCTCTGACACAGCACTATGATCATGAACTGGAAATTTTCAATGTCGTGGACA	542
615	TTGGATTTGGGGTGGGATTTGTCCTGTTTATCTCTATGCTTTTATTTCTTCCAGCA	674
543	TCATATCTCTGTGCCAGATCAACATTTTATCTCTTATGAGGTTCACTTCTCTCCAGCA	602
675	TTTCCGGGTAGTTTGTCTGAGGGGAGGTCTAAAGCCTTCAATGCTGACGCTCTTACA	734
603	TTTTCACATCAACTCCATAGAGGGAGGTCCAGAGCCTTACAGACCGTCAAGTTCACACA	662
735	TAATTTGAGTTCTCTTTCTTTGGGTGAGGAGTTTAAAGTACTCAAAACCCCTTCCA	794
663	TAATTTGAGTTCTCTCTTTTGCATAGGATGATTAATATCTTAAACCTTCTCTCAG	722

QY 795 TTT 797
Db 723 TTT 725

RESULT 15
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LOCUS BZ281255 848 bp DNA linear GSS 15-OCT-2002
DEFINITION CH230-344K8, TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
ACCESSION BZ281255
VERSION BZ281255.1 GI:2408451
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 848)
Zhao, S., Shetty, J., Shatsman, S., Tseng, G., Geer, K.,
Shivarte, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, P., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Other GSSs: CH230-344K8, TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ordering information.htm). BAC end
plate: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 344 row: K column: 8
Seq primer: 17
Class: BAC ends.
Location/Qualifiers
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/clone="CH230-344K8"
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/note="Vector: pTRBAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SNHsd/MCM) BAC library produced by
Pieter de Jong"

ORIGIN
Query Match 34.6%; Score 333.2; DB 28; Length 848;
Best Local Similarity 68.1%; Pred. No. 8.2e-69;
Matches 492; Conservative 0; Mismatches 228; Indels 2; Gaps 2;

QY 211 TTTAGTTCTCTAGACATCATTCCTCAAAATGCTGATGCTTTGCTCAAGAGAA 270
Db 1 TCTCTGCTATCTACTGCTGCTCACTCCAAAATGCTGATGCTTTGCTCAAGAGAA 60
QY 271 CATATTTCTCTACAGGGGTGATGAGTCTTCTCTCTCTGTTCTTTGCTTTTC 330
Db 61 TGCATTTCTTACATGGAGTGTGACCAAGCTATATTTCTTTGTTTGTGCAATTC 120
QY 331 TGAATCTTCACTCTGTGGGAGTGTGAGAGACCGCTACCTGGGCACTGTAAACCACT 390
Db 121 TGAATGTATGTGTGATCTCAATGGCTTATGATGCTTTGTGGCACTCTTAATCCACT 180
QY 391 GTTGACAGATCAACCATGCTCTCCCAAGGTGTGTTGCTCTTTACTGGGATGCTACGG 450

Db 181 TTTGTACATGTTGCCATCTCCCTAAATGTGTGTAACCTTATGCTGGACATATTT 240
QY 451 GATGGGGGTTTTGGGGCTGTGGCTCATACAGAAATATAGTTTCTACCTTTTGGC 510
Db 241 AATGCAATTTCTGTGGCCATGCTCACAGAGATGATGCTAAAGTACCTTCTGTGA 300
QY 511 AGACAACCTTGTCATCACTACATGATGACATCTTCCCTTCTGTGAGCTCTCTGCA 570
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QY 571 CGGCTCTCAATAAATGCTGCTCATCTTTATGTTGAGCGTGGCATGGGGTGGC 630
Db 361 CAGACCTTATGTCATGAATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 631 CATTTGCGCTTTTATCTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTT 690
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QY 691 TGTGAGGCGAGTCTTAAGCTTCAATGCTGAGCTTCTTCAATATTTGAGTTTCT 750
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Db 541 GTTCTTGGATCAGTGATTTATGATTTATGATTTATGATTTATGATTTATGATTT 600
QY 811 GGGGAAGTGTCT 870
Db 601 AGAAAAAACCCTTCTGATTTTATTAACCAATGTTGTTCTTATGATGATTC-TTATCTA 659
QY 871 CAGCTGAGGAATTAAGATGTCAAACTTGCCCTGAAGAGAACTTTCCAGATTAAGCT 930
Db 660 CAG-TTAAGGAGCAAAAGATGTAAATAATGCGCTGAGAAACTCTGATGAGCAATT 718
QY 931 TT 932
Db 719 TT 720

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Job time : 3090 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 01:24:18 ; Search time 4162 Seconds

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Searched: 3470272 seqs, 21671516995 residues

Word size : 20

Total number of hits satisfying chosen parameters: 606

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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41: em_hugo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	963	100.0	AX555964	AX555964 Sequence
2	912	94.7	AC083958	AC083958 Homo sapi
3	912	94.7	AP000916	AP000916 Homo sapi
4	911	94.6	AX241500	AX241500 Sequence
5	706	73.3	AX646877	AX646877 Sequence
6	289	30.0	AY448475	AY448475 Gorilla g
7	224	23.3	AR427386	AR427386 Sequence
8	224	23.3	BD122939	BD122939 EST and e
9	133	13.8	AY448357	AY448357 Hylobates
10	121	12.6	AX646875	AX646875 Sequence
11	121	12.6	AX241493	AX241493 Sequence
12	121	12.6	AY448924	AY448924 Cercopit
13	77	8.0	AY449293	AY449293 Saimiri s
14	67	7.0	AY448835	AY448836 Callithr
15	57	5.9	AX181578	AX181578 Sequence
16	57	5.9	AF179842	AF179842 Saimiri b
17	53	5.5	AY448503	AY448503 Alouatta
18	53	5.5	AY448759	AY448759 Cercocebu
19	43	4.5	SCO233799	AJ233799 Stenella
20	41	4.3	AC096935	AC096935 Rattus no
21	39	4.0	AX181571	AX181571 Sequence
22	39	4.0	AF179838	AF179838 Saimiri b
23	39	4.0	AX181511	AX181511 Sequence
24	39	4.0	AX181560	AX181560 Sequence
25	39	4.0	AF179805	AF179805 Callithr
26	39	4.0	AF179832	AF179832 Saimiri s
27	39	4.0	AX181491	AX181491 Sequence
28	39	4.0	AF179793	AF179793 Macaca sy
29	39	4.0	AX181525	AX181525 Sequence
30	39	4.0	AF179812	AF179812 Pongo pyg
31	39	4.0	AF399511	AF399511 Homo sapi
32	39	4.0	AY449228	AY449228 Ateles fu
33	39	4.0	AY448895	AY448895 Cercopit
34	39	4.0	AX242246	AX242246 Sequence
35	39	4.0	AX244609	AX244609 Sequence
36	39	4.0	AX448443	AX448443 Sequence
37	39	4.0	BD144473	BD144473 Novel G-P
38	39	4.0	AX554459	AX554459 Sequence
39	39	4.0	AX556206	AX556206 Sequence
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44	39	4.0	AP001524	AP001524 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS AX555964
DEFINITION Sequence 23 from Patent WO0250275.
ACCESSION AX555964
VERSION AX555964.1 GI:25899399
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Padigaru, M., Kekuda, R., Li, L., Ballinger, R.A., Casman, S.J.,
Spytek, K.A., Baumgartner, J.C., and Burgess, C.B.
TITLE Novel proteins and nucleic acids encoding same

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http://ftp.genome.washington.edu/RM/RepeatMasker.html
Genome Center
Center: Whitehead Institute / MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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Project Information
Center project name: U1149
Center clone name: 16_M5
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Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 16811 bases at least Q40
Consensus quality: 170912 bases at least Q30
Consensus quality: 171602 bases at least Q20
Insert size: 176000; agarose-ftp
Insert size: 172291; sum-of-contigs
Quality coverage: 7.3 in Q20 bases; agarose-ftp
Quality coverage: 7.4 in Q20 bases; sum-of-contigs

```


JOURNAL Submitted (17-DEC-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: hattori@gs.c.riken.go.jp, URL: http://hsp.gs.c.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170) On Jan 31, 2003 this sequence version replaced gi:15637083.

COMMENT
FEATURES
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1. 192926
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Query Match 94.7%; Score 912; DB 9; Length 192926;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 962; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 102701 AATGCTGCGGAGAACTCCCTCCGTCAGAGTTATCCGAGGCTTATACACCA 102642
QY 61 GCCGGACTCCAGAGTCCCGCTTCTTCTGTTTCTAGGTTCTACGCGTCACGGTGT 120
DB 102641 GCCGGACTCCAGAGTCCCGCTTCTTCTGTTTCTAGGTTCTACGCGTCACGGTGT 102582
QY 121 GGGGAACCTGGGCTGATATCTGATAGGGCTCACTCGCCCTGCAATCCCATGTA 180
DB 102581 GGGGAACCTGGGCTGATATCTGATAGGGCTCACTCGCCCTGCAATCCCATGTA 102522
QY 181 CTTTTCCTCCCTCAACTGCTGCTGCTGATTTAGTTTCTCTACGACCATCATCCCAA 240
DB 102521 CTTTTCCTCCCTCAACTGCTGCTGCTGATTTAGTTTCTCTACGACCATCATCCCAA 102462
QY 241 AATGCTGATGATTTTGTCTCAGAGAAACATTTATCTCTTACAGGGTGTATGAGTCA 300
DB 102461 AATGCTGATGATTTTGTCTCAGAGAAACATTTATCTCTTACAGGGTGTATGAGTCA 102402
QY 301 GTTCTTCTCTCTCTGTTTCTTCTTCTTCTGAGCTTCAATCCGTGAGGAGTGTGA 360
DB 102401 GTTCTTCTCTCTCTGTTTCTTCTTCTTCTGAGCTTCAATCCGTGAGGAGTGTGA 102342
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DB 102341 GGAACCGCTACGTTGGGCACTGTGAACCACTGTTGTACAGATCAATGTCCTCCAGGT 102282
QY 421 GTGTTGCTCTCTTACTGAGGAGTGTACAGGATGGGGTCTTGGGGCTGTGCTATAC 480
DB 102281 GTGTTGCTCTCTTACTGAGGAGTGTGTACAGGATGGGGTCTTGGGGCTGTGCTATAC 102222
QY 481 AGGAATAATGATGTTCTCACTTTTGTGACAGAACCTGTGTCAATCACTACATGTGTGA 540
DB 102221 AGGAATAATGATGTTCTCACTTTTGTGACAGAACCTGTGTCAATCACTACATGTGTGA 102162
QY 541 CATCTTCCTCTGTTGAGGCTCTCTGCAAGGCTCTTACATAATGCTCTGCTCATCTT 600
DB 102161 CATCTTCCTCTGTTGAGGCTCTCTGCAAGGCTCTTACATAATGCTCTGCTCATCTT 102102
QY 601 TATGTTGTGACCGTGGCATTTGGGATGGCCATGTTGCGGTTTATCTCTATGATTT 660
DB 102101 TATGTTGTGACCGTGGCATTTGGGATGGCCATGTTGCGGTTTATCTCTATGATTT 102042
QY 661 TATCTCTTCCAGGATTTCTCCCGCTTATGTTCTGCTGAGGGGAGGTCTTAAGCCTTCAAGT 720
DB 102041 TATCTCTTCCAGGATTTCTCCCGCTTATGTTCTGCTGAGGGGAGGTCTTAAGCCTTCAAGT 101982
QY 721 CTGAGCTCTTACATAATGTCAGATTTCTCTTTCTTGGGTCAGAGGCTTATACGTAACCT 780
DB 101981 CTGAGCTCTTACATAATGTCAGATTTCTCTTTCTTGGGTCAGAGGCTTATACGTAACCT 101922
QY 781 CAAACCCCTTCACTTTTACCCTTGACACAGGGGAAAGTGTCTCTCCTGTTTATACAC 840

DB 101921 CAAACCCCTTCACTTTTACCCTTGACACAGGGGAAAGTGTCTCTCCTGTTTATACAC 101862
QY 841 TGTGATGCCATGTTTATACCATATATCTACGCTTACAGGAAATAGATGTCAACTTGC 900
DB 101861 TGTGATGCCATGTTTATACCATATATCTACGCTTACAGGAAATAGATGTCAACTTGC 101802
QY 901 CTTGAGAGAACCTTTTCCAGAAATATAGCTTTCTGAAAAAATTTAGAAACAGAAAG 960
DB 101801 CTTGAGAGAACCTTTTCCAGAAATATAGCTTTCTGAAAAAATTTAGAAACAGAAAG 101742
QY 961 AGA 963
DB 101741 AGA 101739

RESULT 4
AX241500 994 bp DNA linear PAT 26-SEP-2001
LOCUS Sequence 248 from Patent WO0127158.
ACCESSION AX241500
VERSION AX241500.1 GI:15798375
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 Bellenson, V., Smith, D., Lance, D., Glusman, G., Fuchs, T. and Yanai, I.
TITLE Olfactory receptor sequences
JOURNAL Patent: WO 0127158-A 248 19-Apr-2001;
FEATURES
source
1. 994
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="(H38997 nucleotide)"

Query Match 94.6%; Score 911; DB 6; Length 994;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 961; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGCTGCGGAGAACTCCCTCCGTCAGAGTTATCCGAGGCTTATACACAG 61
DB 1 AATGCTGCGGAGAACTCCCTCCGTCAGAGTTATCCGAGGCTTATACACAG 60
QY 62 CCGGACTCCAGAGTCCCGCTTCTTCTGTTTCTAGGTTTCTACGCGTCAAGTGTG 121
DB 61 CCGGACTCCAGAGTCCCGCTTCTTCTGTTTCTAGGTTTCTACGCGTCAAGTGTG 120
QY 122 GGGAACTGGGCTGATATCTGATAGGCTCAACTGCGCTGCAATCTCCCATGTAC 181
DB 121 GGGAACTGGGCTGATATCTGATAGGCTCAACTGCGCTGCAATCTCCCATGTAC 180
QY 182 TTTTTCCTCCCTCAACTGCTGCTGATGTTTATGTTTCTGAGCAACATATCCCAA 241
DB 181 TTTTTCCTCCCTCAACTGCTGCTGATGTTTATGTTTCTGAGCAACATATCCCAA 240
QY 242 ATGCTGATGATTTTGTCTCAGAGAAACATTTATCTCTTACAGAGGCTGTAGTCA 301
DB 241 ATGCTGATGATTTTGTCTCAGAGAAACATTTATCTCTTACAGAGGCTGTAGTCA 300
QY 302 TTTCTCTCTCTGTTTCTTGTCTTCTTCTGAGCTTCAATCCGTGAGGAGTGTGAG 361
DB 301 TTTCTCTCTCTGTTTCTTGTCTTCTTCTTCTGAGCTTCAATCCGTGAGGAGTGTGAG 360
QY 362 GACCGCTACGTTGGCACTGTGAACCACTGTTGTGAACAGATCAACATGTCTCCCA 421
DB 361 GACCGCTACGTTGGCACTGTGAACCACTGTTGTGAACAGATCAACATGTCTCCCA 420
QY 422 TGTGCTCTCTTACTGAGGAGTGTACAGGAGTGGGGTCTTGGGGCTGTGCTATACA 481

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Db 421 TGTTCCTCCTTTTACTGGGTGTCTACGGGATGGGGGTTTGGGGCTGTGGCTCATACA 480
482 GGAATATATGTTTCTACACCTTTGGACAGAACCTTGCAATCACTATACATGTTGAC 541
481 GGAATATATGTTTCTACACCTTTGGACAGAACCTTGCAATCACTATACATGTTGAC 540
542 ATCTTCCCTCTCTAGAGCTCTCTGCAACAGGCTTTACATTAATGTCTGTGATCTTT 601
541 ATCTTCCCTCTCTAGAGCTCTCTGCAACAGGCTTTACATTAATGTCTGTGATCTTT 600
602 ATTTGTTGACCGTTGGGATTTGGGGTGGCCATTTGTCCTGTTTATCTCTATGTTT 661
601 ATTTGTTGACCGTTGGGATTTGGGGTGGCCATTTGTCCTGTTTATCTCTATGTTT 660
662 ATCTTCCAGCATTTCTCGGCTGTAGTCTGTGAGGAGGCTTAAAGCTTCAGTAGC 721
661 ATCTTCCAGCATTTCTCGGCTGTAGTCTGTGAGGAGGCTTAAAGCTTCAGTAGC 720
722 TGCAGCTCTACATATATGAGTCTCTCTTTCTTTGGGTGAGAGCTTTTACGTACTC 781
721 TGCAGCTCTACATATATGAGTCTCTCTTTCTTTGGGTGAGAGCTTTTACGTACTC 780
782 AAACCCCTTCATTTTACCCCTGACACGAGGAAAGTCTCTCCCTGTTCTATACCACT 841
781 AAACCCCTTCATTTTACCCCTGACACGAGGAAAGTCTCTCCCTGTTCTATACCACT 840
842 GTGTCGCCCATTTTAAACCATTAATCTACAGCTTGAGGAATPAAGATGTCAAATTTGCC 901
841 GTGTCGCCCATTTTAAACCATTAATCTACAGCTTGAGGAATPAAGATGTCAAATTTGCC 900
902 CTGAAGAGAACCTTTCCAGGAATPAAGCTTTCTTGAATAAATTTAGAAAAGAAAAGA 961
901 CTGAAGAGAACCTTTCCAGGAATPAAGCTTTCTTGAATAAATTTAGAAAAGAAAAGA 960
Qy 962 GA 963
Db 961 GA 962

RESULT 5
AX646877 931 bp DNA linear PAT 04-MAR-2003
LOCUS AX646877
DEFINITION Sequence 1069 from Patent EP1270724.
ACCESSION AX646877
VERSION AX646877.1 GI:28799404
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H.
G-protein-coupled receptor kinase-1 (GRK1) is a protein-coupled receptor
kinase. EP 1270724-A 1069 02-JAN-2003;
National Institute of Advanced Industrial Science and Technology
(JP) ; Center for Advanced Science and Technology Incubation, Ltd.
(JP)

FEATURES
Source
1.931
Location/Qualifiers
1.931
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/translaction="MSPOVCLLLGLVYGVGVGAHAHTNIVLFFCADNVLNHYMC
DIPLESCNGSYINVLFIVTVGVIVAVFSTGFIISLIRVSSAAGRSKA
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DVRLAKRTFRISFS"
CDS

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ORIGIN
Query Match 73.3%; Score 706; DB 6; Length 931;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 756; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 207 TAGATTTAGTTTCTCTACGACCATCATTCGCAAAATGCTATGATTTGTCTCAAGA 266
Db 1 TAGATTTAGTTTCTCTACGACCATCATTCGCAAAATGCTATGATTTGTCTCAAGA 60
Qy 267 AGAACATTTATTTCTTACAGGCTGTATGATGATTTCTTTCTTTCTTTCTTTCT 326
Db 61 AGAACATTTATTTCTTACAGGCTGTATGATGATTTCTTTCTTTCTTTCTTTCT 120
Qy 327 TTTCTAGTCTTTCTTACCTCTGCGGCAATGTTGAGGAGACCGCTAGGGGATCTGTAAC 386
Db 121 TTTCTAGTCTTTCTTACCTCTGCGGCAATGTTGAGGAGACCGCTAGGGGATCTGTAAC 180
Qy 387 CACTGTGTACAGATCAGATCAGATCTCTCCAGGATGTTGCTCTTTTACTGGGTGCT 446
Db 181 CACTGTGTACAGATCAGATCAGATCTCTCCAGGATGTTGCTCTTTTACTGGGTGCT 240
Qy 447 ACGGATGCGGGTTTGGGGCTGTGCTCATACAGAAATATAGTTTCTACACCTTT 506
Db 241 ACGGATGCGGGTTTGGGGCTGTGCTCATACAGAAATATAGTTTCTACACCTTT 300
Qy 507 GTGAGACAACTTGTATCATCATCATCATCATCATCATCATCATCATCATCATCATCT 566
Db 301 GTGAGACAACTTGTATCATCATCATCATCATCATCATCATCATCATCATCATCATCT 360
Qy 567 GCAACGGCTCTTACATTAATGTCCTGTGATCTTTATGTTGTTGACCGTTGGG 626
Db 361 GCAACGGCTCTTACATTAATGTCCTGTGATCTTTATGTTGTTGACCGTTGGG 420
Qy 627 TGCCATGTTGGCGTTTATATCTTATGTTTATCTTCTTCAAGATCTCGCGCTTA 686
Db 421 TGCCATGTTGGCGTTTATATCTTATGTTTATCTTCTTCAAGATCTCGCGCTTA 480
Qy 481 GTTCTGAGGAGGAGGCTTAAAGCTTCACTAGCTCAGCTCTCATTAATGCACTTT 746
Db 481 GTTCTGAGGAGGAGGCTTAAAGCTTCACTAGCTCAGCTCTCATTAATGCACTTT 540
Qy 747 CTCTTTTCTTTGGGTGAGGACTTTTACGATCTTAAACCCCTTCATTTTACCCCTGG 806
Db 541 CTCTTTTCTTTGGGTGAGGACTTTTACGATCTTAAACCCCTTCATTTTACCCCTGG 600
Qy 807 ACCAGGGGAAAGTGTCTCTCTCTTCTATACAGCTGTGTCCTCATGTTTAAACCATTA 866
Db 601 ACCAGGGGAAAGTGTCTCTCTCTTCTATACAGCTGTGTCCTCATGTTTAAACCATTA 660
Qy 867 TCTACAGCTTGAAGATATGATGTCAAATCTTGGCTTGAAGAACTTTTCCAGATTA 926
Db 661 TCTACAGCTTGAAGATATGATGTCAAATCTTGGCTTGAAGAACTTTTCCAGATTA 720
Qy 927 GCTTTCTTGAATAAATTTTGAAGAGAAAGA 963
Db 721 GCTTTCTTGAATAAATTTTGAAGAGAAAGA 757

RESULT 6
AY448475 667 bp DNA linear PRI 07-DEC-2003
LOCUS AY448475
DEFINITION Gorilla gorilla clone OLG_68 olfactory receptor-like protein gene,
partial sequence.
ACCESSION AY448475
VERSION AY448475.1 GI:38634503
KEYWORDS
SOURCE Gorilla gorilla (gorilla)
ORGANISM Gorilla gorilla
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
REFERENCE
1 (bases 1 to 667)
Giles, Y., Wiebe, V., Przeworski, M., Lancel, D. and Paabo, S.

```

TITLE
Loss of olfactory receptor genes coupled with the acquisition of full trichromatic vision in primates

JOURNAL
Unpublished

REFERENCE
2 (bases 1 to 667)

AUTHORS
Gillad, Y., Wiebe, V., Przeworski, M., Lancel, D. and Paabo, S.

TITLE
Submitted (20-OCT-2003) Max Plank Institute for Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103, Germany

FEATURES
source
1. .667
/organism="gorilla gorilla"
/mol_type="genomic DNA"
/db_xref="taxon:9593"
/clone="OLG.68"
/note="sample obtained from Primate Genetics German Primate Center in Goettingen, Germany"
/gene="olfactory receptor-like protein"

ORIGIN
Query Match 30.0%; Score 289; DB 9; Length 667;
Best Local Similarity 100.0%; Pred. No. 1.2e-147; Indels 0; Gaps 0;
Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 CTTTACTGGGTGTCTACGGATGGGGTTTGGGGCTGCTCATACAGAAATXA 490
DB 242 CTTTACTGGGTGTCTACGGATGGGGTTTGGGGCTGCTCATACAGAAATATA 301
QY 491 GTGTTTCACCTTTTGGGACAGACCTTGTCATCTCATGTGTGACATCCTTCCC 550
DB 302 GTGTTTCACCTTTTGGGACAGACCTTGTCATCTCATGTGTGACATCCTTCCC 361
QY 551 CTTTCTGAGCTCTCTGACAGAGCTCTTACATAATGCTGTCATCTTATTTGTGTG 610
DB 362 CTTTCTGAGCTCTCTGACAGAGCTCTTACATAATGCTGTCATCTTATTTGTGTG 421
QY 611 ACCGTTGGCATTGGGGTCCCATTTGTCCTTTTATCTTATGTTTATCTTCC 670
DB 422 ACCGTTGGCATTGGGGTCCCATTTGTCCTTTTATCTTATGTTTATCTTCC 481
QY 671 AGCATTTCCCGGTAGTTGCTGAGAGGAGGCTTAAGCCTTCAGTA 719
DB 482 AGCATTTCCCGGTAGTTGCTGAGAGGAGGCTTAAGCCTTCAGTA 530

RESULT 7
AA427386/c 485 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION
Sequence 18883 from patent US 6639063.
ACCESSION
AA427386
VERSION
AA427386.1 GI:40182496
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 485)
AUTHORS
Edwards, J.-B.D.M., Robert, S. and Giordano, J.-Y.
TITLE
EST's and encoded human proteins
JOURNAL
Patent: US 6639063-A 18883 28-OCT-2003;
FEATURES
source
1. .485
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 23.3%; Score 224; DB 6; Length 485;
Best Local Similarity 100.0%; Pred. No. 1e-111; Indels 0; Gaps 0;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 402 TCACCAATGCTCCCGAGAGTGTGCTCTTTTACTAGGCTCTACGGATGGGGGTTT 461
DB 265 TCACCAATGCTCCCGAGAGTGTGCTCTTTTACTAGGCTCTACGGATGGGGGTTT 206

QY 462 TTGGGGCTGTGCTCATACAGAAATATAGTTTCTACACCTTTTGGACAGACACTTG 521
DB 205 TTGGGGCTGTGCTCATACAGAAATATAGTTTCTACACCTTTTGGACAGACACTTG 146
QY 522 TCATCTCATGTCATGTGAGATCTTCCCTTTCTTGAAGCTCTCTGCAAGGCTTTACA 581
DB 145 TCATCTCATGTCATGTGAGATCTTCCCTTTCTTGAAGCTCTCTGCAAGGCTTTACA 86
QY 582 TAAATGCTGTCATCTTATTTGTTGTGACCGTGGCATTTGG 625
DB 85 TAAATGCTGTCATCTTATTTGTTGTGACCGTGGCATTTGG 42

RESULT 8
BD122939/c 485 bp DNA linear PAT 18-SEP-2002
LOCUS
DEFINITION
EST and encoded human protein.
ACCESSION
BD122939
VERSION
BD122939.1 GI:23217884
KEYWORDS
JP 2002010789-A/15016.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 485)
AUTHORS
Edwards, J.B.D.M., Robert, S. and Giordano, J.E.
TITLE
EST and encoded human protein
JOURNAL
Patent: JP 2002010789-A 15016 15-JAN-2002;
COMMENT
GENSET CORP
OS Homo sapiens (human)
PN JP 2002010789-A/15016
PD 15-JAN-2002
PF 07-AUG-2002 JP 2002080989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
C12N15/00
CC EST and encoded human protein
FT Key
FT source
FT 1. .485
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/db_xref="taxon:9606"

ORIGIN
Query Match 23.3%; Score 224; DB 6; Length 485;
Best Local Similarity 100.0%; Pred. No. 1e-111; Indels 0; Gaps 0;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 402 TCACCAATGCTCCCGAGAGTGTGCTCTTTTACTAGGCTCTACGGATGGGGGTTT 461
DB 265 TCACCAATGCTCCCGAGAGTGTGCTCTTTTACTAGGCTCTACGGATGGGGGTTT 206
QY 462 TTGGGGCTGTGCTCATACAGAAATATAGTTTCTACACCTTTTGGACAGACACTTG 521
DB 205 TTGGGGCTGTGCTCATACAGAAATATAGTTTCTACACCTTTTGGACAGACACTTG 146
QY 522 TCATCTCATGTCATGTGAGATCTTCCCTTTCTTGAAGCTCTCTGCAAGGCTTTACA 581
DB 145 TCATCTCATGTCATGTGAGATCTTCCCTTTCTTGAAGCTCTCTGCAAGGCTTTACA 86
QY 582 TAAATGCTGTCATCTTATTTGTTGTGACCGTGGCATTTGG 625
DB 85 TAAATGCTGTCATCTTATTTGTTGTGACCGTGGCATTTGG 42

RESULT 9

AY448357
LOCUS 668 bp DNA linear PRI 07-DEC-2003
DEFINITION Hylobates syndactylus clone OLG_29 olfactory receptor-like protein
ACCESSION AY448357
VERSION AY448357.1 GI:38634385
KEYWORDS
SOURCE Hylobates syndactylus (slamang)
ORGANISM Hylobates syndactylus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hylodactylidae; Hylobates.
REFERENCE 1 (bases 1 to 668)
Gild, Y., Wiebe, V., Przeworski, M., Lancet, D. and Paabo, S.
Loss of olfactory receptor genes coupled with the acquisition of full trichromatic vision in primates
JOURNAL Unpublished
AUTHORS Gild, Y., Wiebe, V., Przeworski, M., Lancet, D. and Paabo, S.
TITLE Direct Submission
JOURNAL Submitted (20-OCT-2003) Max Planck Institute for Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103, Germany
FEATURES
source
1. 668
/organism="Hylobates syndactylus"
/mol_type="genomic DNA"
/db_xref="taxon:9590"
/clone="OLG_29"
/note="sample obtained from Primate Genetics German Primate Center in Goettingen, Germany"
<1..>668
/gene="olfactory receptor-like protein"
ORIGIN
Query Match 13.8%; Score 133; DB 9; Length 668;
Best Local Similarity 100.0%; Pred. No. 1.9e-61;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 482 GGAAATATGCTTTCTCAGCTTTTGTGAGACACACCTTGATACATCACTGATGATAC 541
DB 293 GGAAATATGCTTTCTCAGCTTTTGTGAGACACACCTTGATACATCACTGATGATAC 352
QY 542 ATCTTCCCTCTTGTAGCTCTCTGCAACGCTCTTACATTAATGCTCTGTCATCTTT 601
DB 353 ATCTTCCCTCTTGTAGCTCTCTGCAACGCTCTTACATTAATGCTCTGTCATCTTT 412
QY 602 ATTGTTGTGACCG 614
DB 413 ATTGTTGTGACCG 425
RESULT 10
AX646875 886 bp DNA linear PAT 04-MAR-2003
LOCUS
DEFINITION Sequence 1067 from Patent EP1270724.
ACCESSION AX646875
VERSION AX646875.1 GI:28799398
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H.
Guanosine triphosphate-binding protein coupled receptors
Patent: EP 1270724-A, 1067 02-JUN-2003;
National Institute of Advanced Science and Technology Incubation, Ltd.
(JP)
FEATURES
source
1. 886
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Location/Qualifiers

CDS
201..686
/note="unnamed protein product"
/codon_start=1
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/db_xref="REFSEQ:CAD69564"
/translation="MEAKNSSTTATITSLDQDQLOIPAFELFGFAVTVVGNLGLIILIGNSRLHLMVTFPPNLSFIDFSITLAPKMLSPSENISTISLGLMTLWPCFVFVSESYILSAMAYDRYVGINPLLYVTWSPQMCULLLGLVGMGLGLMTWET"
ORIGIN
Query Match 12.6%; Score 121; DB 6; Length 886;
Best Local Similarity 100.0%; Pred. No. 8.2e-55;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 82 CTCTCTCTGTTTCTAGATTCTACGGGCTACGGGTGTTGGGGAACCTGGGCTTGAAT 141
DB 281 CTCTCTCTGTTTCTAGATTCTACGGGCTACGGGTGTTGGGGAACCTGGGCTTGAAT 340
QY 142 CCGATATGGGCTCACTCTGCGCTGCATATCCCATGACTTTTCCCTTCAACTGTC 201
DB 341 CCGATATGGGCTCACTCTGCGCTGCATATCCCATGACTTTTCCCTTCAACTGTC 400
QY 202 C 202
DB 401 C 401
RESULT 11
AX241493 935 bp DNA linear PAT 26-SEP-2001
LOCUS
DEFINITION Sequence 241 from Patent WO0127158.
ACCESSION AX241493
VERSION AX241493.1 GI:15798368
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
Bellenson, J., Smith, D., Lancet, D., Glusman, G., Fuchs, T. and Yanai, I.
TITLE Olfactory receptor sequences
JOURNAL Patent: WO 0127158-A, 241 19-APR-2001;
Dissequences (US) / YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)
FEATURES
source
1. 935
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="(H38990 nucleotide)"
ORIGIN
Query Match 12.6%; Score 121; DB 6; Length 935;
Best Local Similarity 100.0%; Pred. No. 8.1e-55;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 82 CTCTCTCTGTTTCTAGATTCTACGGGCTACGGGTGTTGGGGAACCTGGGCTTGAAT 141
DB 81 CTCTCTCTGTTTCTAGATTCTACGGGCTACGGGTGTTGGGGAACCTGGGCTTGAAT 140
QY 142 CCGATATGGGCTCACTCTGCGCTGCATATCCCATGACTTTTCCCTTCAACTGTC 201
DB 141 CCGATATGGGCTCACTCTGCGCTGCATATCCCATGACTTTTCCCTTCAACTGTC 200
QY 202 C 202
DB 201 C 201
RESULT 12
AY448924 667 bp DNA linear PRI 07-DEC-2003
LOCUS


```

DEFINITION Cercopithecus aethiops clone OLG_7 olfactory receptor-like protein
ACCESSION AY448924
VERSION AY448924.1 GI:38634952
KEYWORDS
SOURCE
ORGANISM Cercopithecus aethiops (African green monkey)
REFERENCE
AUTHORS Gildad,Y., Wiebe,V., Przeworski,M., Lancet,D. and Paabo,S.
TITLE Loss of olfactory receptor genes coupled with the acquisition of
full trichromatic vision in primates
JOURNAL Unpublished
REFERENCE
AUTHORS Gildad,Y., Wiebe,V., Przeworski,M., Lancet,D. and Paabo,S.
TITLE Loss of olfactory receptor genes coupled with the acquisition of
full trichromatic vision in primates
JOURNAL Unpublished
FEATURES
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/organism="Cercopithecus aethiops"
/mol_type="genomic DNA"
/db_xref="taxon:9534"
/clone="OLG 7"
/note="sample obtained from Primate Genetics German
Primate Center in Goettingen, Germany"
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/gene="Olfactory receptor-like protein"

ORIGIN
Query Match 8.0%; Score 77; DB 9; Length 667;
Best Local Similarity 100.0%; Pred. No. 1,7e-30;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 491 GTGTTTCACCTTTGTGACAGACCTTGTCAATCAATGATGTCATCCTTCCC 550
DB 302 GTGTTTCACCTTTGTGACAGACCTTGTCAATCAATGATGTCATCCTTCCC 361
QY 551 CTCTTGAGCTCTCCTG 567
DB 362 CTCTTGAGCTCTCCTG 378

RESULT 13
LOCUS AY449293 667 bp DNA linear PRI 07-DEC-2003
DEFINITION Saimiri sciureus clone OLG_66 olfactory receptor-like protein gene,
partial sequence.
ACCESSION AY449293
VERSION AY449293.1 GI:38635321
KEYWORDS
SOURCE
ORGANISM Saimiri sciureus (common squirrel monkey)
REFERENCE
AUTHORS Gildad,Y., Wiebe,V., Przeworski,M., Lancet,D. and Paabo,S.
TITLE Loss of olfactory receptor genes coupled with the acquisition of
full trichromatic vision in primates
JOURNAL Unpublished
REFERENCE
AUTHORS Gildad,Y., Wiebe,V., Przeworski,M., Lancet,D. and Paabo,S.
TITLE Loss of olfactory receptor genes coupled with the acquisition of
full trichromatic vision in primates
JOURNAL Unpublished
FEATURES
SOURCE
1..667
/organism="Saimiri sciureus"
/mol_type="genomic DNA"
/db_xref="taxon:9521"

DEFINITION Cercopithecus aethiops clone OLG_66 olfactory receptor-like protein
ACCESSION AY448924
VERSION AY448924.1 GI:38634952
KEYWORDS
SOURCE
ORGANISM Cercopithecus aethiops (African green monkey)
REFERENCE
AUTHORS Gildad,Y., Wiebe,V., Przeworski,M., Lancet,D. and Paabo,S.
TITLE Loss of olfactory receptor genes coupled with the acquisition of
full trichromatic vision in primates
JOURNAL Unpublished
REFERENCE
AUTHORS Gildad,Y., Wiebe,V., Przeworski,M., Lancet,D. and Paabo,S.
TITLE Loss of olfactory receptor genes coupled with the acquisition of
full trichromatic vision in primates
JOURNAL Unpublished
FEATURES
SOURCE
1..667
/organism="Cercopithecus aethiops"
/mol_type="genomic DNA"
/db_xref="taxon:9534"
/clone="OLG 7"
/note="sample obtained from Primate Genetics German
Primate Center in Goettingen, Germany"
<1..>667
/gene="Olfactory receptor-like protein"

ORIGIN
Query Match 8.0%; Score 77; DB 9; Length 667;
Best Local Similarity 100.0%; Pred. No. 1,7e-30;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 491 GTGTTTCACCTTTGTGACAGACCTTGTCAATCAATGATGTCATCCTTCCC 550
DB 302 GTGTTTCACCTTTGTGACAGACCTTGTCAATCAATGATGTCATCCTTCCC 361
QY 551 CTCTTGAGCTCTCCTG 567
DB 362 CTCTTGAGCTCTCCTG 378

RESULT 14
LOCUS AY448836 668 bp DNA linear PRI 07-DEC-2003
DEFINITION Callithrix jacchus clone OLG_58 olfactory receptor-like protein
gene, partial sequence.
ACCESSION AY448836
VERSION AY448836.1 GI:38634864
KEYWORDS
SOURCE
ORGANISM Callithrix jacchus (white-tufted-ear marmoset)
REFERENCE
AUTHORS Gildad,Y., Wiebe,V., Przeworski,M., Lancet,D. and Paabo,S.
TITLE Loss of olfactory receptor genes coupled with the acquisition of
full trichromatic vision in primates
JOURNAL Unpublished
REFERENCE
AUTHORS Gildad,Y., Wiebe,V., Przeworski,M., Lancet,D. and Paabo,S.
TITLE Loss of olfactory receptor genes coupled with the acquisition of
full trichromatic vision in primates
JOURNAL Unpublished
FEATURES
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Best Local Similarity 100.0%; Pred. No. 5.8e-25;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 ATCATTCCTCAAAATGCTGATGATTTGTCCTCAAGAGAAATATTTCTTCACAGGG 269
DB 41 ATCATTCCTCAAAATGCTGATGATTTGTCCTCAAGAGAAATATTTCTTCACAGGG 100
QY 290 TGTATGA 296
DB 101 TGTATGA 107

RESULT 15
LOCUS AX181578 487 bp DNA linear PAT 07-AUG-2001
DEFINITION Sequence 366 from Patent WO0146262.
ACCESSION AX181578

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VERSION      AX181578.1  GI:15141666
KEYWORDS
SOURCE
ORGANISM      Saimiri boliviensis (Bolivian squirrel monkey)
               Saimiri boliviensis
               Saimiri boliviensis
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae;
               Saimiri.
REFERENCE
1
AUTHORS      Rouquier, S. and Giorgi, D.
TITLE        Olfactory receptor genes and pseudogenes in primates and mouse
JOURNAL      Patent: WO 0146262-A 366 28-JUN-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
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ORIGIN
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Search completed: September 30, 2004, 07:22:58
Job time : 4167 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments) 8685.806 Million cell updates/sec

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 20

Total number of hits satisfying chosen parameters: 151

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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8: genebegn2003bs:*
9: genebegn2003cs:*
10: genebegn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	963	100.0	963 6 AAF88413	Aah18413 Human GPC
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5	121	12.6	886 9 ADC86614	ADC86614 Human GPC
6	121	12.6	886 9 AAh1568	Aah1568 Human GPC
7	57	5.9	467 4 AAh84099	Aah84099 Mouse olf
8	39	4.0	466 4 AAh84095	Aah84095 Mouse olf
9	39	4.0	467 4 AAh84062	Aah84062 Fongu pyg
10	39	4.0	487 4 AAh84089	Aah84089 Salimiri b
11	39	4.0	489 4 AAh84050	Aah84050 Macaca sy
12	39	4.0	489 4 AAh84069	Aah84069 Pongo pyg
13	39	4.0	930 4 AAh12421	Aah12421 Human olf
14	39	4.0	933 5 AAh15910	Aah15910 DNA encod
15	39	4.0	933 5 AAh42233	Aah42233 Human GPC
16	39	4.0	933 5 AAh243067	Aah243067 Human GPC
17	39	4.0	933 6 AAh68455	Aah68455 Human DNA
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19	39	4.0	933 6 AAh7521	Aah7521 DNA encod
20	39	4.0	976 6 AAh97207	Aah97207 Human G-P
21	39	4.0	976 6 AAh50328	Aah50328 Human G-P
22	39	4.0	991 6 AAh58782	Aah58782 Human G-P
23	39	4.0	1333 9 AAh5838	Aah5838 Human GPC

24	39	4.0	1655 6 AAd24449	Aad24449 Human G-P
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26	33	3.4	486 4 AAh84022	Aah84022 Eulemar f
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31	33	3.4	951 6 AAh68456	Aah68456 Human DNA
32	33	3.4	989 6 AAh58834	Aah58834 Human GPC
33	33	3.4	1336 6 AAh68200	Aah68200 Human GPC
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37	28	2.9	950 6 AAd12838	Aad12838 DNA encod
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39	28	2.9	962 6 AAd12840	Aad12840 DNA encod
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43	26	2.7	951 6 AAh68432	Aah68432 Human DNA
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ALIGNMENTS

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XX	12-NOV-2002 (first entry)	
DT	12-NOV-2002 (first entry)	
XX	Human GPCX CDNA SEQ ID 23.	
XX	Human, anti-HIV; nootropic; antilactamic; antiarteriosclerotic; GPCX;	
KW	Human, anti-HIV; nootropic; antilactamic; antiarteriosclerotic; GPCX;	
KW	immunodysplastic; immunomodulator; cytosolic; antiinflammatory; AIDS;	
KW	antidiabetic; neuroprotective; anorectic; haemostatic; antibacterial;	
KW	fungicide; protozoal; virucide; human G-protein coupled receptor;	
KW	gene therapy; vaccine; cardiomyopathy; atherosclerosis; diabetes;	
KW	cell signal processing; cancer; obesity; neurodegenerative disorder;	
KW	cachexia; anorexia; Alzheimer's disease; Parkinson's disease;	
KW	immune disorder; graft versus host disease; bronchial asthma;	
KW	Crohn's disease; multiple sclerosis; haemophilia; infectious disease;	
KW	idiopathic thrombocytopenic purpura; gene; ss.	
XX	Homo sapiens.	
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XX	WO200250275-A2.	
XX	27-JUN-2002.	
PD	18-DEC-2001; 2001WC-US048958.	
XX	18-DEC-2001; 2001WC-US048958.	
XX	18-DEC-2000; 2000US-0256635P.	
PR	21-DEC-2000; 2000US-0256635P.	
PR	04-JAN-2001; 2001US-0259743P.	
PR	10-JAN-2001; 2001US-0260718P.	
PR	12-JAN-2001; 2001US-0261498P.	
PR	24-JAN-2001; 2001US-0263689P.	
PR	08-FEB-2001; 2001US-0267464P.	
PR	22-FEB-2001; 2001US-0271021P.	
PR	14-MAR-2001; 2001US-0275946P.	
PR	23-MAR-2001; 2001US-0278150P.	
PR	18-APR-2001; 2001US-0284591P.	
PR	23-APR-2001; 2001US-0285718P.	
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PR	16-AUG-2001; 2001US-0312902P.	
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QY	61	GCGGAGCTCCAGGTCCCGCTTCTCTCTGTTCCTAGGTTTCAACGGGATCAAGTGGT	120
Dp	61	GCGGAGACTCCAGGTCCCGCTTCTCTCTGTTCCTAGGTTTCAACGGGATCAAGTGGT	120
QY	121	GGGGAACCTGGGCTTGATATACCTATATAGGGTCAACCTGGCTGCATATCCCCATGTA	180
Dp	121	GGGGAACCTGGGCTTGATATACCTATATAGGGTCAACCTGGCTGCATATCCCCATGTA	180
QY	181	CTTTTCCCGCTCAACTGTGCCCTGATGATTAGTTCTCTACAGACATATCCCAA	240
Dp	181	CTTTTCCCGCTCAACTGTGCCCTGATGATTAGTTCTCTACAGACATATCCCAA	240
QY	241	AATGCTGATGATTTTGTCTCAAGAGAACATATATTCCTTCCACAGGTTGTAAGTCA	300
Dp	241	AATGCTGATGATTTTGTCTCAAGAGAACATATATTCCTTCCACAGGTTGTAAGTCA	300
QY	301	GTTCTCTCTCTCTGTTTCTTGTGTTTTCAGACCTTCATCCGTTGGGAGATGGTGGGA	360
Dp	301	GTTCTCTCTCTCTGTTTCTTGTGTTTTCAGACCTTCATCCGTTGGGAGATGGTGGGA	360
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DR WPI; 2001-290713/30.
 XX New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists.
 XX
 XX
 PS Claim 8; Page 276; 1857bp; English.
 XX
 The present sequence is one of a number of isolated polynucleotides which
 CC encode polypeptides involved in olfactory sensation. The polynucleotides
 CC can be used in screening for olfactory agonists and antagonists. The
 CC methods allow for the determination of primary scents and the
 CC identification of the odor receptors used to detect these primary
 CC scents. The methods also enable determination of secondary scents and the
 CC identification of combinations of odor receptors that are involved in
 CC detecting such secondary scents. This enables the construction of a scent
 CC representation (also called a scent fingerprint or scent profile), which
 CC may be used to re-create and edit scents. Libraries of olfactory
 CC receptors are useful for determining the interaction pattern of a
 CC composition with the receptors, and can be used for determining
 CC differences in the olfactory faculties of different individuals
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 SQ Sequence 994 BP; 201 A; 250 C; 207 G; 336 T; 0 U; 0 Other;
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 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 961; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ATGCTGCGGAGAACTCTCTCCGTGAGAGATTATCCGAGGCTTAATCCAGCAG 61
 DB 1 ATGCTGCGGAGAACTCTCTCCGTGAGAGATTATCCGAGGCTTAATCCAGCAG 60
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 DB 61 CCGGAGCTCCAGGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
 QY 122 GGGAACTGGGCTGATATCCGATGAGGCTCACTCGGCTGATATCCGATGATAC 181
 DB 121 GGGAACTGGGCTGATATCCGATGAGGCTCACTCGGCTGATATCCGATGATAC 180
 QY 182 TTTTCCCTTCACTGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241
 DB 181 TTTTCCCTTCACTGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
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 DB 301 TTCTTCTTCTCTGTTTCTTGTCTTCTTCTGAGTCTCTTCACTCGTCTGGCGAGTGTAG 360
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 DB 781 AAACCCCTTCCATTTTACCCCTGAGACAGGGAAGTGTCTCTCTCTATACACT 840
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 DB 841 GTGTGCTCCATGTTTAACTCAATTAATGATGAGGCTGAGATGCAATCTGCC 900
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 XX 01-JAN-2004 (first entry)
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 KW ds; gene; human; GPCR;
 KW guanosine triphosphate-binding protein coupled receptor; gene therapy.
 OS Homo sapiens.
 XX
 XX BP1270724-A2.
 XX
 XX 02-JAN-2003.
 PD
 XX 18-JUN-2002; 2002EP-00013517.
 PF
 XX 18-JUN-2001; 2001JP-00246789.
 PR
 XX
 XX (NAND-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (AUSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 PI Suwa M, Aseai K, Akiyama Y, Aburatani H;
 DR WPI; 2003-315783/31.
 DR P-PSDB; ADCC8617.
 PT New polynucleotide, useful for preparing a composition for treating a
 PT patient in need of increased or suppressed activity or expression of the
 PT guanosine triphosphate-binding protein coupled receptor.
 XX
 XX
 PS Claim 1; SEQ ID NO 1069; 28bp; English.
 XX
 XX The invention relates to a novel polynucleotide encoding a guanosine
 CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
 CC the invention may have a use in gene therapy. The polynucleotide and
 CC polypeptide are useful for preparing a composition for treating a patient
 CC in need of increased or suppressed activity or expression of the
 CC guanosine triphosphate-binding protein coupled receptor. The
 CC polynucleotide sequences shown in ADCC85548-ADCC87616 encode GPCR's of the
 CC invention.
 SQ Sequence 931 BP; 202 A; 215 C; 180 G; 334 T; 0 U; 0 Other;
 Query Match 73.3%; Score 706; DB 9; Length 931;
 Best Local Similarity 99.9%; Pred. No. 0;

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Db	61	GCCGGGACTCCAGTCCCGCTCTTCTCTGTTTCTAGGTTTCTACGGGCTACAGTGGT	120
OY	121	GGGGAACTGGGCTGTAATCCGTATAGGGCTCAACTCGGCTGCAATATCCCATGTA	180
Db	121	GGGGAACTGGGCTGTAATCCGTATAGGGCTCAACTCGGCTGCAATATCCCATGTA	180
OY	181	CTTTTCCCTTCAACTGTGCTCCGTAGATTTAAGTTCTCTACGACCACTCATCCCA	240
Db	181	CTTTTCCCTTCAACTGTGCTCCGTAGATTTAAGTTCTCTACGACCACTCATCCCA	240
OY	241	AATGCTATAGTTTTGTCTCAAGGAAACAATTATTCCTTCCACAGGGGTATAGTCA	300
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OY	361	GGACCGCTAGTGGGCACTGTACACCACTGTGTACAGACACACATGTCTCCCAAGT	420
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Db	538	CATCTTCCTCCCTCTTAGGCTCTCTGCAAGGCTCTTACATTAATGTCTGATCATCTT	597
OY	601	TATGTGTGACCGGTGGCATTTGGGAGCCCATGTGTCCGTTTATCTTAATGTTTT	660
Db	598	TATGTGTGACCGGTGGCATTTGGGAGCCCATGTGTGTCCGTTTATCTTAATGTTTT	657
OY	661	TATCTTTCAGAACTCCGGGTTAGTCTGTAGGGGAGGCTTAAGGCTTCAAGTAG	720
Db	658	TATCTTTCAGAACTCCGGGTTAGTCTGTAGGGGAGGCTTAAAGCTTCAAGTAG	717
OY	721	CTGAGCTCTACATAATGCAATTTCTTTTCTTTGGGTAGAGGCTTTTACGTACT	780
Db	718	CTGAGCTCTACATAATGCAATTTCTTTTCTTTGGGTAGAGGCTTTTACGTACT	777
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Db	778	CAAAACCCCTTCCATTTTACCTCTGGACCAAGGGGAAAAGTCTCTCCCTGTCTATACAC	837
OY	841	TGTGTGCCCATGTTTAACCATTAATCTACAGCCTGAGAAATAGAGATGTCAACTTGC	900
Db	838	TGTGTGCCCATGTTTAACCATTAATCTACAGCCTGAGAAATAGAGATGTCAACTTGC	897
OY	901	CTTGAAGGAACCTTTTCCAGAAATAGCTTTTCTTGAATAAATTTTGGAAACGAAAG	960
Db	898	CCTGAAGGAACCTTTTCCAGAAATAGCTTTTCTTGAATAAATTTTGGAAACGAAAG	957
OY	961	AGA 963	
Db	958	AGA 960	

XX OS Homo sapiens.
 XX PN WO200127158-A2.
 XX PD 19-APR-2001.
 XX PF 06-OCT-2000; 2000WO-US027582.
 XX PR 08-OCT-1999; 99US-0158615P.
 XX PR 24-FEB-2000; 2000US-0184809P.
 XX PA (DIGI-) DIGISCENTS.
 XX PA (YEDA) YEDA RES & DEV CO LTD.
 XX PI Belenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
 XX DR WPI; 2001-290713/30.
 XX PT New polynucleotides which encode polypeptides involved in olfactory
 XX PT sensation for identifying olfactory agonists and antagonists.
 XX PS Claim 8; Page 273; 1857pp; English.
 XX CC The present sequence is one of a number of isolated polynucleotides which
 CC encode polypeptides involved in olfactory sensation. The polynucleotides
 CC can be used in screening for olfactory agonists and antagonists. The
 CC methods allow for the determination of primary scents and the
 CC identification of the odour receptors used to detect these primary
 CC scents. The methods also enable determination of secondary scents and the
 CC identification of combinations of odour receptors that are involved in
 CC detecting such secondary scents. This enables the construction of a scent
 CC representation (also called a scent fingerprint or scent profile), which
 CC may be used to re-create and edit scents. Libraries of olfactory
 CC receptors are useful for determining the interaction pattern of a
 CC composition with the receptors, and can be used for determining
 CC differences in the olfactory faculties of different individuals
 XX SQ Sequence 935 BP; 189 A; 238 C; 190 G; 318 T; 0 U; 0 Other;
 Query Match 12.6%; Score 121; DB 4; Length 935;
 Best Local Similarity 100.0%; Pred. No. 3.1e-50;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 82 CTCTCTCTGTTTCTAGGTTTCTACGGCGTACGGTGGGGAAGCTGGGCTTGATAT 141
 DB 81 CTCTCTCTGTTTCTAGGTTTCTACGGCGTACGGTGGGGAAGCTGGGCTTGATAT 140
 QY 142 CCGATAGGGCTCAACTCTCGCGTCGATATCCCATGACTTTTCCCTTCAACTGTC 201
 DB 141 CCGATAGGGCTCAACTCTCGCGTCGATATCCCATGACTTTTCCCTTCAACTGTC 200
 QY 202 C 202
 DB 201 C 201
 RESULT 7
 AAH84099
 ID AAH84099 standard; DNA; 487 BP.
 XX AC AAH84099;
 XX DT 25-SEP-2001 (first entry)
 XX DE Mouse olfactory receptor encoding gene 6.
 XX KM Olfactory receptor; primate; mouse; human; food processing industry;
 XX KM aromas; perfumery; toxic substance; ds.
 XX OS Mus musculus domesticus.
 XX PN WO200146262-A2.

XX PD 28-JUN-2001.
 XX PF 22-DEC-2000; 2000WO-IB002017.
 XX PR 22-DEC-1999; 99US-0171746P.
 XX PR 21-DEC-2000; 2000US-00747155.
 XX PA (CNRS) CNRS CENT NAT RECH SCI.
 XX PI Rouquier S, Giorgi D;
 XX DR WPI; 2001-381911/40.
 XX DR P-PSDB; AAG98584.
 XX PT Nucleic acids encoding primate and murine olfactory receptors, useful for
 XX PT analysis odors e.g. in food processing and perfumery.
 XX PS Claim 1; Page 415-416; 482pp; English.
 XX CC The invention relates to olfactory receptors (AAG98432-AAG98609) and the
 CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
 CC primate species, mouse and human. The nucleic acids and receptors may be
 CC used in the food processing industry (e.g. for the detection of aromas,
 CC quality control and sample analysis), in perfumery (e.g. for the analysis
 CC or comparison of perfumes) and in the environment (e.g. for the detection
 CC of toxic substances and/or trapping of odours)
 XX SQ Sequence 487 BP; 86 A; 120 C; 105 G; 176 T; 0 U; 0 Other;
 Query Match 5.9%; Score 57; DB 4; Length 487;
 Best Local Similarity 100.0%; Pred. No. 4.9e-18;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 514 CAACCTTGACATCACTACATGTGACATCCCTCCCTTGAGCTCTCGCAA 570
 DB 145 CAACCTTGACATCACTACATGTGACATCCCTCCCTTGAGCTCTCTCGCAA 201
 RESULT 8
 AAH84095
 ID AAH84095 standard; DNA; 486 BP.
 XX AC AAH84095;
 XX DT 25-SEP-2001 (first entry)
 XX DE Mouse olfactory receptor encoding gene 2.
 XX KM Olfactory receptor; primate; mouse; human; food processing industry;
 XX KM aromas; perfumery; toxic substance; ds.
 XX OS Mus musculus domesticus.
 XX OS PN WO200146262-A2.
 XX PD 28-JUN-2001.
 XX PF 22-DEC-2000; 2000WO-IB002017.
 XX PR 22-DEC-1999; 99US-0171746P.
 XX PR 21-DEC-2000; 2000US-00747155.
 XX PA (CNRS) CNRS CENT NAT RECH SCI.
 XX PI Rouquier S, Giorgi D;
 XX DR WPI; 2001-381911/40.
 XX DR P-PSDB; AAG98580.
 XX PT Nucleic acids encoding primate and murine olfactory receptors, useful for
 XX PT analysis odors e.g. in food processing and perfumery.

PS Claim 1; Page 405-406; 482pp; English.

XX CC The invention relates to olfactory receptors (AG98432-AG98609) and the
 CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
 CC primate species, mouse and human. The nucleic acids and receptors may be
 CC used in the food processing industry (e.g. for the detection of aromas,
 CC quality control and sample analysis), in perfumery (e.g. for the analysis
 CC or comparison of perfumes) and in the environment (e.g. for the detection
 CC of toxic substances and/or trapping of odours)

SQ Sequence 486 BP; 92 A; 114 C; 105 G; 175 T; 0 U; 0 Other;

Query Match 4.0%; Score 39; DB 4; Length 486;
 Best Local Similarity 100.0%; Pred. No. 5.6e-09;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 642 TTTTATCTCTTATGCTTTATCTTTCAGCATTTCTCC 680
 DB 273 TTTTATCTCTTATGCTTTATCTTTCAGCATTTCTCC 311

RESULT 9
 ID AAH84062 standard; DNA; 487 BP.
 XX AC AAH84062;
 XX XX
 DT 25-SEP-2001 (first entry)
 XX PI
 DE Pongo pygmaeus olfactory receptor pseudogene 10.
 XX XX
 KM Olfactory receptor; primate; mouse; human; food processing industry;
 KM aromas; perfumery; toxic substance; ds.
 XX OS Pongo pygmaeus.
 PN WO200146262-A2.
 XX PD 28-JUN-2001.
 XX PF 22-DEC-2000; 2000WO-1B002017.
 XX PR 22-DEC-1999; 99US-0171746P.
 XX PR 21-DEC-2000; 2000US-00747155.
 XX PA (CNRS) CNRS CENT NAT RECH SCI.
 XX PI Rouquier S, Giorgi D;
 DR WPI; 2001-381911/40.
 XX PT Nucleic acids encoding primate and murine olfactory receptors, useful for
 XX PT analysis odors e.g. in food processing and perfumery.
 PS Claim 1; Page 347-348; 482pp; English.

XX CC The invention relates to olfactory receptors (AG98432-AG98609) and the
 CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
 CC primate species, mouse and human. The nucleic acids and receptors may be
 CC used in the food processing industry (e.g. for the detection of aromas,
 CC quality control and sample analysis), in perfumery (e.g. for the analysis
 CC or comparison of perfumes) and in the environment (e.g. for the detection
 CC of toxic substances and/or trapping of odours)

SQ Sequence 487 BP; 88 A; 118 C; 107 G; 174 T; 0 U; 0 Other;

Query Match 4.0%; Score 39; DB 4; Length 487;
 Best Local Similarity 100.0%; Pred. No. 5.6e-09;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 642 TTTTATCTCTTATGCTTTTATCTTTCAGCATTTCTCC 680
 DB 273 TTTTATCTCTTATGCTTTTATCTTTCAGCATTTCTCC 311

RESULT 10
 ID AAH84089 standard; DNA; 487 BP.
 XX AC AAH84089;
 XX XX
 DT 25-SEP-2001 (first entry)
 XX PI
 DE Salmiiri boliviensis olfactory receptor encoding gene 11.
 XX XX
 KM Olfactory receptor; primate; mouse; human; food processing industry;
 KM aromas; perfumery; toxic substance; ds.
 XX OS Salmiiri boliviensis.
 PN WO200146262-A2.
 XX PD 28-JUN-2001.
 XX PF 22-DEC-2000; 2000WO-1B002017.
 XX PR 22-DEC-1999; 99US-0171746P.
 XX PR 21-DEC-2000; 2000US-00747155.
 XX PA (CNRS) CNRS CENT NAT RECH SCI.
 XX PI Rouquier S, Giorgi D;
 DR WPI; 2001-381911/40.
 DR P-PSDB; AG98575.
 XX PT Nucleic acids encoding primate and murine olfactory receptors, useful for
 XX PT analysis odors e.g. in food processing and perfumery.
 XX OS
 PS Claim 1; Page 394-395; 482pp; English.

XX CC The invention relates to olfactory receptors (AG98432-AG98609) and the
 CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
 CC primate species, mouse and human. The nucleic acids and receptors may be
 CC used in the food processing industry (e.g. for the detection of aromas,
 CC quality control and sample analysis), in perfumery (e.g. for the analysis
 CC or comparison of perfumes) and in the environment (e.g. for the detection
 CC of toxic substances and/or trapping of odours)

SQ Sequence 487 BP; 92 A; 116 C; 105 G; 174 T; 0 U; 0 Other;

Query Match 4.0%; Score 39; DB 4; Length 487;
 Best Local Similarity 100.0%; Pred. No. 5.6e-09;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 642 TTTTATCTCTTATGCTTTTATCTTTCAGCATTTCTCC 680
 DB 273 TTTTATCTCTTATGCTTTTATCTTTCAGCATTTCTCC 311

RESULT 11
 ID AAH84050 standard; DNA; 489 BP.
 XX AC AAH84050;
 XX XX
 DT 25-SEP-2001 (first entry)
 XX PI
 DE Macaca sylvanus olfactory receptor pseudogene 6.
 XX XX
 KM Olfactory receptor; primate; mouse; human; food processing industry;
 KM aromas; perfumery; toxic substance; ds.
 XX OS Macaca sylvanus.
 PN WO200146262-A2.

```

XX 28-JUN-2001.
PD
XX
PF 22-DEC-2000; 2000MO-IB002017.
XX
XX 22-DEC-1999; 99US-0171746P.
PR 21-DEC-2000; 2000US-00747155.
XX
PA (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI Rouquier S, Giorgi D;
XX
DR WPI; 2001-381911/40.
XX
PT Nucleic acids encoding primate and murine olfactory receptors, useful for
XX analysis odors e.g. in food processing and perfumery.
XX
PS Claim 1; Page 326; 482pp; English.
XX
XX The invention relates to olfactory receptors (AA398432-AA398609) and the
CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
CC primate species, mouse and human. The nucleic acids and receptors may be
CC used in the food processing industry (e.g. for the detection of aromas,
CC quality control and sample analysis), in perfumery (e.g. for the analysis
CC or comparison of perfumes) and in the environment (e.g. for the detection
CC of toxic substances and/or trapping of odours)
XX
SQ Sequence 489 BP; 95 A; 120 C; 104 G; 170 T; 0 U; 0 Other;

Query Match          4.0%; Score 39; DB 4; Length 489;
Best Local Similarity 100.0%; Pred. No. 5.6e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 642 TTTTATCTCTTATGTTTATCTTTCAGCATTCCTCC 680
    |||||
DB 273 TTTTATCTCTTATGTTTATCTTTCAGCATTCCTCC 311

RESULT 12
AAH84069
ID AAH84069 standard; DNA; 491 BP.
XX
AC AAH84069;
XX
DT 25-SEP-2001 (first entry)
XX
DE Pongo pygmaeus olfactory receptor pseudogene 13.
XX
KM Olfactory receptor; primate; mouse; human; food processing industry;
XX aromas; perfumery; toxic substance; ds.
XX
OS Pongo pygmaeus.
XX
XX WO200146262-A2.
XX
PD 28-JUN-2001.
XX
PF 22-DEC-2000; 2000MO-IB002017.
XX
XX 22-DEC-1999; 99US-0171746P.
PR 21-DEC-2000; 2000US-00747155.
XX
PA (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI Rouquier S, Giorgi D;
XX
DR WPI; 2001-381911/40.
XX
PT Nucleic acids encoding primate and murine olfactory receptors, useful for
XX analysis odors e.g. in food processing and perfumery.
XX
PS Claim 1; Page 357-358; 482pp; English.
XX

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CC The invention relates to olfactory receptors (AA398432-AA398609) and the
CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
CC primate species, mouse and human. The nucleic acids and receptors may be
CC used in the food processing industry (e.g. for the detection of aromas,
CC quality control and sample analysis), in perfumery (e.g. for the analysis
CC or comparison of perfumes) and in the environment (e.g. for the detection
CC of toxic substances and/or trapping of odours)
XX
SQ Sequence 491 BP; 92 A; 118 C; 105 G; 176 T; 0 U; 0 Other;

Query Match          4.0%; Score 39; DB 4; Length 491;
Best Local Similarity 100.0%; Pred. No. 5.6e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 642 TTTTATCTCTTATGTTTATCTTTCAGCATTCCTCC 680
    |||||
DB 273 TTTTATCTCTTATGTTTATCTTTCAGCATTCCTCC 311

RESULT 13
AAH32421
ID AAH32421 standard; DNA; 930 BP.
XX
AC AAH32421;
XX
DT 30-JUN-2001 (first entry)
XX
DE Human olfactory receptor polynucleotide, SEQ ID NO: 994.
XX
KM Human; olfactory receptor; OR; primary scent determination;
XX secondary scent determination; polypeptide library; odour receptor;
XX scent profile; scent fingerprint; scent representation; ds.
XX
OS Homo sapiens.
XX
XX NO200127158-A2.
XX
PD 19-APR-2001.
XX
PF 06-OCT-2000; 2000MO-US027582.
XX
PR 08-OCT-1999; 99US-0156615P.
XX 24-FEB-2000; 2000US-0184809P.
XX
PA (DIGI-) DIGISCENTS.
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX
DR WPI; 2001-290713/30.
XX
PT New polynucleotides which encode polypeptides involved in olfactory
XX sensation for identifying olfactory agonists and antagonists.
XX
PS Claim 8; Page 577; 1857pp; English.
XX
XX The present sequence is one of a number of isolated polynucleotides which
CC encode polypeptides involved in olfactory sensation. The polynucleotides
CC can be used in screening for olfactory agonists and antagonists. The
CC methods allow for the determination of primary scents and the
CC identification of the odour receptors used to detect these primary
CC scents. The methods also enable determination of secondary scents and
CC identification of combinations of odour receptors that are involved in
CC detecting such secondary scents. This enables the construction of a scent
CC representation (also called a scent fingerprint or scent profile), which
CC may be used to re-create and edit scents. Libraries of olfactory
CC receptors are useful for determining the interaction pattern of a
CC composition with the receptors, and can be used for determining
CC differences in the olfactory faculties of different individuals
XX
SQ Sequence 930 BP; 190 A; 251 C; 188 G; 301 T; 0 U; 0 Other;

Query Match          4.0%; Score 39; DB 4; Length 930;

```

Best Local Similarity 100.0%; Pred. No. 5.7e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 TCCCAAAATGCTGATGATTGTTCTCAAGGAAGAACAT 273
231 TCCCAAAATGCTGATGATTGTTCTCAAGGAAGAACAT 269

RESULT 14
AAS15910
ID AAS15910 standard; cDNA; 933 BP.
AC AAS15910;
XX
XX 25-JAN-2002 (first entry)
XX
XX
XX DNA encoding G-protein coupled receptor (GCREC) #14.
DE
XX G-protein coupled receptor; GCREC; vaccine; gene therapy;
XX cell proliferation disorder; cancer; arteriosclerosis;
XX neurologic disorder; epilepsy; stroke; cardiovascular disorder;
XX hypertension; ischaemic heart disease; gastrointestinal disorder;
XX anorexia; peptic ulcer; autoimmune disorder; inflammatory disorder;
XX diabetes; osteoporosis; psoriasis; metabolic disorder; obesity;
XX schizophrenia disorder; neuroskeletal disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1. .933
FT CDS /*tag= a
FT /product= "GCREC 14"
FT /note= "G-protein coupled receptor 14"

WO200166742-A2.
13-SEP-2001.
01-MAR-2001; 2001MO-US006814.
XX
XX 03-MAR-2000; 2000US-0186854P.
XX 10-MAR-2000; 2000US-0188384P.
XX 17-MAR-2000; 2000US-0190453P.
XX 20-MAR-2000; 2000US-0190730P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Lal P, Tang YT, Patterson C, Yao MG, Shih LL, Tribouley CM;
XX Lu DM, Yue H, Khan FA, Policky JL, Au-Young J, Yang J, Harland L;
XX Walsh RT, Lo TP, Borowsky ML;
XX
XX WPI; 2001-656776/75.
XX P-PSDB; AAU10313.
XX
XX Novel G-protein coupled receptor polypeptides, for treating and
XX preventing autoimmune/inflammatory disorders, neurological disorders,
XX cell proliferative disorders, cardiovascular disorders and viral
XX infections.
XX
XX Claim 5; Page 138; 141pp; English.

The invention describes a novel isolated polypeptide, selected from a group of 21 G-protein coupled receptor polypeptides (GCREC) and useful in vaccines and gene therapy. The polypeptide (I) is useful for screening for agonist or antagonist of (I), compounds specifically binding to (I), or compounds that modulate the activity of (I). The polynucleotide encoding (I) is useful for screening a compound for effectiveness in altering expression of a target polynucleotide comprising (II), by exposing a sample comprising the target polynucleotide to a compound, detecting altered expression of the target polynucleotide, and comparing the expression of the target polynucleotide in the presence of varying amounts of compound and in the absence of the compound. (I) and (II) are useful for diagnosis, treatment and prevention of cell proliferative

disorders (e.g. cancers, arteriosclerosis, atherosclerosis), neurological disorders (e.g. epilepsy, stroke, schizophrenic disorders and neuroskeletal disorders), cardiovascular disorders (e.g. hypertension, ischaemic heart disease), gastrointestinal disorders (e.g. anorexia, peptic ulcer, autoimmune/inflammatory disorders (e.g. diabetes mellitus, osteoporosis, psoriasis), and metabolic disorders such as obesity). Furthermore, the polynucleotide is useful as primers for detecting single nucleotide polymorphisms; as elements in microarray, to monitor or measure protein-protein interactions, drug-target interactions, and gene expression profiles; to generate a transcript image of a tissue or cell type, and to generate hybridisation probes useful in mapping the naturally occurring genomic sequence. This sequence encodes G-protein coupled receptor 14, one of 21 GCREC proteins described in the method of the invention

Sequence 933 BP; 192 A; 251 C; 188 G; 302 T; 0 U; 0 Other;

Query Match 4.0%; Score 39; DB 5; Length 933;
Best Local Similarity 100.0%; Pred. No. 5.7e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 TCCCAAAATGCTGATGATTGTTCTCAAGGAAGAACAT 273
231 TCCCAAAATGCTGATGATTGTTCTCAAGGAAGAACAT 269

RESULT 15
AAS42233
ID AAS42233 standard; cDNA; 933 BP.
AC AAS42233;
XX
XX 18-DEC-2001 (first entry)
XX
XX
XX Human CDNA encoding olfactory receptor AOLF25.
DE
XX Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;
XX ss; food additive; cosmetic; fragrance; pharmaceutical additive.
XX
XX Homo sapiens.
OS
XX
XX WO200168805-A2.
XX
XX 20-SEP-2001.
XX
XX 13-MAR-2001; 2001MO-US007771.
XX
XX 13-MAR-2000; 2000US-0188914P.
XX 24-MAR-2000; 2000US-0192033P.
XX 12-APR-2000; 2000US-0198474P.
XX 24-APR-2000; 2000US-0199335P.
XX 26-MAY-2000; 2000US-0207702P.
XX 23-JUN-2000; 2000US-0213849P.
XX 16-AUG-2000; 2000US-0226534P.
XX 07-SEP-2000; 2000US-0230732P.
XX 07-FEB-2001; 2001US-026862P.
XX
XX (SENO-) SENOMYX INC.
XX
XX Zozulya S;
XX
XX WPI; 2001-570867/64.
XX P-PSDB; AAU24540.
XX
XX Nucleic acids encoding human olfactory G protein-coupled receptors,
XX useful for screening for compounds involved in olfactory sensation, where
XX the compounds can be used in the food, pharmaceutical and cosmetic
XX industries to customize odors.
XX
XX Claim 1; Page 94; 319pp; English.
XX
XX The invention relates to nucleic acids encoding human olfactory
XX receptors, OR, (a G protein-coupled receptor, GPCR). The OR's

CC specifically recognise molecules, odourants, that elicit specific
CC olfactory sensation. The human olfactory receptors and polynucleotides
CC encoding them are useful for screening a library of chemical compounds
CC for compounds that are involved in olfactory sensation. Modulators of
CC their activity are useful for pharmacological and genetic modulation of
CC olfactory signalling pathways. Therefore, they can be used in the food,
CC pharmaceutical and cosmetic industries to customise odours and
CC fragrances. The present sequence encodes a human olfactory receptor of
CC the invention
XX
SQ Sequence 933 BP; 192 A; 251 C; 188 G; 302 T; 0 U; 0 Other;
Query Match 4.0%; Score 39; DB 5; Length 933;
Best Local Similarity 100.0%; Pred. No. 5.7e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 235 TCCCAAAATGCTGATGAGTTTGTCTCAAGAGAAACAT 273
Db 231 TCCCAAAATGCTGATGAGTTTGTCTCAAGAGAAACAT 269

Search completed: September 30, 2004, 06:13:28
Job time : 4/74 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 04:40:49 ; Search time 3087 seconds

(without alignments)
9315.607 Million cell updates/sec

Title: US-10-023-597-23

Perfect score: 963
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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 segs, 14931090276 residues

Word size : 20

Total number of hits satisfying chosen parameters: 201

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estbm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_hiv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	4.0	799	29	AY407110 Pan trogl
2	39	4.0	933	29	AY407109 Homo sapi
3	33	3.4	903	29	AY405609 Homo sapi
4	31	3.2	605	14	CB174014 OR_2031G0

Result No.	Score	Query Match	Length	DB ID	Description
5	30	3.1	504	14	CB174105
6	28	2.9	456	12	BI274717
7	28	2.9	560	14	CB173336
8	28	2.9	683	28	AO31094
9	26	2.7	442	14	CA681328
10	26	2.7	472	14	CA680338
11	26	2.7	452	28	BO4945
12	26	2.7	877	28	BH418698
13	26	2.7	903	29	AY405611
14	26	2.7	933	29	AY407111
15	25	2.6	625	29	CE158635
16	24	2.5	504	29	CE243689
17	24	2.5	683	13	BY720370
18	24	2.5	899	29	AY405610
19	23	2.4	334	10	BF444685
20	23	2.4	334	10	AM486191
21	23	2.4	359	13	BY024438
22	23	2.4	387	14	CB173998
23	23	2.4	387	28	BZ949576
24	23	2.4	392	14	CB173314
25	23	2.4	451	12	BI399100
26	23	2.4	455	28	AZ080621
27	23	2.4	475	28	AZ016145
28	23	2.4	496	13	AM431124
29	23	2.4	652	14	CB440691
30	23	2.4	931	29	CNS07980
31	23	2.4	962	29	CNS07761
32	23	2.4	985	29	CNS07981
33	23	2.4	1066	29	CNS076WC
34	23	2.4	1201	9	AL539244
35	22	2.3	259	13	BO451234
36	22	2.3	267	10	BB049231
37	22	2.3	394	14	CB173920
38	22	2.3	414	13	BO451187
39	22	2.3	423	13	BO577021
40	22	2.3	432	12	BI670687
41	22	2.3	445	14	CB173642
42	22	2.3	454	14	CB173295
43	22	2.3	463	13	BU498696
44	22	2.3	473	14	CB173023
45	22	2.3	535	13	BU497196

ALIGNMENTS

RESULT 1
AY407110
LOCUS
DEFINITION Pan troglodytes ORB12 gene, VIRTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
ACCESSION
AY407110
KEYWORDS
SOURCE
ORGANISM
Pan troglodytes (chimpanzee)
REFERENCE
AY407110.1 GI:39763081
AUTHORS
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 799)
AUTHORS
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES
 source location/Qualifiers
 1..799
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 <1..>799
 /gene="OR8B12"
 /locus_tag="HGM2781"

ORIGIN

Query Match 4.0%; Score 39; DB 29; Length 799;
 Best Local Similarity 100.0%; Pred. No. 6.9e-09;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 235 TCCCAAAATGCTGATGATTTGCTCTCAAGAGAACAT 273
 |||||
 Db 231 TCCCAAAATGCTGATGATTTGCTCTCAAGAGAACAT 269

RESULT 2
 AY407109 933 bp DNA linear GSS 15-DEC-2003
 LOCUS Homo sapiens OR8B12 gene, VIRTUAL TRANSCRIPT, partial sequence.
 DEFINITION
 ACCESSION AY407109.1 GI:39763080
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 933)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 Science 302 (5652), 1960-1963 (2003)
 14671302
 2 (bases 1 to 933)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES
 source location/Qualifiers
 1..933
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 <1..>933
 /gene="OR8B12"
 /locus_tag="HGM2781"

ORIGIN

Query Match 4.0%; Score 39; DB 29; Length 933;
 Best Local Similarity 100.0%; Pred. No. 6.9e-09;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 235 TCCCAAAATGCTGATGATTTGCTCTCAAGAGAACAT 273
 |||||
 Db 231 TCCCAAAATGCTGATGATTTGCTCTCAAGAGAACAT 269

RESULT 3
 AY405609 903 bp DNA linear GSS 16-DEC-2003
 LOCUS Homo sapiens OR8B8 gene, VIRTUAL TRANSCRIPT, partial sequence.
 DEFINITION
 ACCESSION AY405609.1 GI:39761583
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 903)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 Science 302 (5652), 1960-1963 (2003)
 14671302
 2 (bases 1 to 903)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES
 source location/Qualifiers
 1..903
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 <1..>903
 /gene="OR8B8"
 /locus_tag="HGM2281"

ORIGIN

Query Match 3.4%; Score 33; DB 29; Length 903;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 527 CACTACATGTGTGACATCCTTCCCTTCTTGTAG 559
 |||||
 Db 493 CACTACATGTGTGACATCCTTCCCTTCTTGTAG 525

RESULT 4
 CB174014 605 bp mRNA linear EST 09-OCT-2003
 LOCUS OR 2031G09.010529.y1 Adult mouse olfactory epithelium library Mus musculus cDNA clone 2031G09 5', mRNA sequence.
 DEFINITION
 ACCESSION CB174014.1 GI:37592643
 VERSION
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriongnathi; Muridae; Murine; Mus.
 REFERENCE
 1 (bases 1 to 605)
 Young,J.M., Shykind,B.M., Lane,R.P., Tonnes-Priddy,L., Ross,J.A., Walker,M., Williams,E.M. and Traak,B.J.
 Odorant receptor expressed sequence tags demonstrate olfactory expression of over 400 genes, extensive alternate splicing and unequal expression levels
 Genome Biol. 4 (11), R71.1-R71.15 (2003)
 Contact: Young JM
 Trask Lab, Division of Human Biology
 Fred Hutchinson Cancer Research Center
 1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA

98109-1024, USA
Tel: 206 667 1471
Fax: 206 667 6524
Email: jayoung@hcr.org
Young gene new name GA_X6K02T2PVT-32841223-32842158
Young gene old name GA_X5J8B7W60AJ-489886-489890
Other gene name K9
Zhang gene name MOR171-6
Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers
1..605
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="2031009"
/issue_type="olfactory and respiratory epithelium"
/dev_stage="Adult"
/clone_lib="Adult mouse olfactory epithelium library"
/note="Organ: Olfactory turbinates; Vector: LambdaZAPII-XR; Site 1: EcoRI; Site 2: XhoI; This library was provided by Leslie Voeshall. mRNA was prepared from the olfactory and respiratory epithelium of an adult mouse. Oligo-dT primed cDNA was directionally cloned into Stratagene's LambdaZAPII-XR vector."

ORIGIN

Query Match 3.2%; Score 31; DB 14; Length 605;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 863 TTATCTACAGCCTGAGGATTAAGATGTCA 893
DB 504 TTATCTACAGCCTGAGGATTAAGATGTCA 534

RESULT 5

CB174105 504 bp mRNA linear EST 09-OCT-2003
LOCUS OR_2034C01.010615.y1 Adult mouse olfactory epithelium library Mus
DEFINITION musculus cDNA clone 2034C01 5', mRNA sequence.
CB174105
ACCESSION CB174105.1 GI:37592734
VERSION 1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 504)
Young, J.M., Shykind, B.M., Lane, R.P., Tonnes-Priddy, L., Ross, J.A., Walker, M., Williams, E.M. and Trask, B.J.
Olfactory receptor expressed sequence tags demonstrate olfactory expression of over 400 genes, extensive alternate splicing and unequal expression levels
Genome Biol. 4 (11), R71.1-R71.15 (2003)
unequal expression levels

TITLE Trask Lab, Division of Human Biology
Fred Hutchinson Cancer Research Center
1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA
98109-1024, USA
Tel: 206 667 1471
Fax: 206 667 6524
Email: jayoung@hcr.org
Young gene new name GA_X6K02T2PVT-33470347-33469403
Young gene old name GA_X5J8B7W3MPH-108802-107858
Zhang gene name MOR171-15
Seq primer: M13 Reverse.

JOURNAL
COMMENT Location/Qualifiers
1..504
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="2034C01"
/issue_type="Olfactory and respiratory epithelium"

FEATURES

source
Location/Qualifiers
1..504
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="2034C01"
/issue_type="Olfactory and respiratory epithelium"

ORIGIN

Query Match 3.1%; Score 30; DB 14; Length 504;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 ATCTACAGCCTGAGGATTAAGATGTCAA 895
DB 342 ATCTACAGCCTGAGGATTAAGATGTCAA 371

RESULT 6
B1274717/c 456 bp mRNA linear EST 18-JUN-2001
LOCUS UI-R-CX0-bxd-b-11-0-UI.s1 UI-R-CX0 Rattus norvegicus cDNA clone
DEFINITION UI-R-CX0-bxd-b-11-0-UI 3', mRNA sequence.
B1274717
ACCESSION B1274717.1 GI:14885894
VERSION 1
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE
AUTHORS 1 (bases 1 to 456)
Bonaldi, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE 9704447
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized rat placenta pool library cDNA library preparation: M.B. Soares Lab Gene distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-48,
>AT rich#low complexity
Seq primer: M13 Forward
POLY-A=yes

FEATURES

source
Location/Qualifiers
1..456
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CX0-bxd-b-11-0-UI"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-CX0"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CX0 library is a normalized library constructed from the following rat placenta tissues: embryonic day 17, embryonic day 19, embryonic day 21. For a detailed

description of the library from which this clone was derived, please visit our web site at ratelst.eng.uiowa.edu. The subtraction has been previously described in (Donald, Lennon and Soares, Genome Research 6:791-806, 1996)

TAG TISSUE=rat placenta pool
TAG_LIB=UI-R-CX0
TAG_SEQ=TCACGACAGT"

ORIGIN

Query Match 2.9%; Score 28; DB 12; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 ATCTACAGCCTGAGGAATAGAGTGTCA 893
DB 303 ATCTACAGCCTGAGGAATAGAGTGTCA 276

RESULT 7
CB173336 560 bp mRNA linear EST 09-OCT-2003
LOCUS OR2016G01.C04_001130_27.Y1 Adult mouse olfactory epithelium
DEFINITION library Mus musculus cDNA clone 2016G01 5', mRNA sequence.
CB173336
ACCESSION CB173336
VERSION CB173336.1 GI:37591965
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; 1 (bases 1 to 560)
Young, J.M., Shykina, E.M., Lane, R.P., Tomes-Priddy, L., Ross, J.A., Walker, M., Williams, E.M. and Traak, B.J.

TITLE
Odorant receptor expressed sequence tags demonstrate olfactory expression of over 400 genes, extensive alternate splicing and unequal expression levels

JOURNAL
COMMENT Genome Biol. 4 (11), R11.1-R11.15 (2003)
Contact: Young JM
Track Lab, Division of Human Biology
Fred Hutchinson Cancer Research Center
1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA 98109-1024, USA
Tel: 206 667 1471
Fax: 206 667 6524
Email: jayoung@fhcrc.org

Young gene new name GA_X6K02T2PMTD-32935684-32934749
Young gene old name GA_X5J8B7SUS4-727-5
Young gene old name GA_X5J8B7W6DAJ-401357-402240

Other gene name K4
Zhang gene name MOR171-32P
Zhang gene name MOR171-41P
Seg primer: M13 Reverse.

FEATURES
source Location/Qualifiers
1..560

/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="2016G01"
/tissue_type="Olfactory and respiratory epithelium"
/dev_stage="Adult"
/clone_lib="Adult mouse olfactory epithelium library"
/note="Organ: Olfactory turbinates; Vector: LambdaZAPRI-XR; Site_1: EcoRI; Site_2: XhoI; This library was provided by Leslie Voshall. mRNA was prepared from the olfactory and respiratory epithelium of an adult mouse. Oligo-dT primed cDNA was directionally cloned into Stratagene's lambdaZAPRI-XR vector."

ORIGIN

Query Match 2.9%; Score 28; DB 14; Length 560;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 ATCTACAGCCTGAGGAATAGAGTGTCA 893
DB 327 ATCTACAGCCTGAGGAATAGAGTGTCA 354

RESULT 8
A0931094 683 bp DNA linear GSS 21-DEC-1999
LOCUS RPCI-23-283118.TV RPCI-23 Mus musculus genomic clone
DEFINITION RPCI-23-283118, genomic survey sequence.
A0931094
ACCESSION A0931094
VERSION A0931094.1 GI:6620106
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; 1 (bases 1 to 683)
Zhao, S., Nieman, W., Feiblyum, T., Malek, J., Shatman, S., Akintet, B., Levin, M., McGann, S., Tsegaye, G., Geer, K., Kol, M., de Jong, P. and Fraser, C.M.

TITLE
JOURNAL Mouse BAC End Sequences from Library RPCI-23
COMMENT Unpublished (1999)
Other GSSs: RPCI-23-283118.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@jlong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea Ch Genetics (<http://www.rchgen.com>). BAC end page: http://www.tigr.org/tdb/bac/ends/mouse/bac_end_intro.html
plate: 283 row: L column: 18
Seg primer: Sp6
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..683

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-283118"
/sex="Female"
/lab_host="DH10B"
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methyase. Site selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

Query Match 2.9%; Score 28; DB 28; Length 683;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 ATCTACAGCCTGAGGAATAGAGTGTCA 893
DB 71 ATCTACAGCCTGAGGAATAGAGTGTCA 98

RESULT 9
CA881328/c 444 bp mRNA linear EST 20-DEC-2002
LOCUS CA881328
DEFINITION K0989F04-5N NTA Mouse Neural Stem Cell (Undifferentiated) cDNA

Library (Long) Mus musculus cDNA clone NIA:K0989F04 IMAGE:30092799
5', mRNA sequence.
ACCESSION CA861328
VERSION CA861328.1 GI:27332877
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 444)
AUTHORS Piao, Y., Dudekula, D.B., Qian, Y., Martin, P.R., Alpa, K., Vescovi, A.L. and Ko, M.S.H.
TITLE Systematic Analyses of NIA Mouse Neural Stem Cell (Undifferentiated) cDNA Library (Long)
JOURNAL Unpublished (2002)
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: K0989 row: F column: 04
Seq primer: -21M13 Reverse
High quality sequence stop: 444
POLYA=No.

FEATURES
source
1. .444
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CD1"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="NIA:K0989F04 IMAGE:30092799"
/dev_stage="Adult"
/lab_host="DH108"
/lab_host="DH108"
/clone_lib="NIA Mouse Neural Stem Cell (Undifferentiated) cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Dr. Angelo L. Vescovi (Institute for Stem Cell Research, Italy). Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTCTAGATCGAGCGCGCCCTTTTCTTTT-3'] from 2.0 Microgram of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lona-linker LL-SalI, purified by phenol/chloroform, and separated from free linkers by centrifugation 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and centrifugation 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH108 E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.8 kb. The library was constructed by Yulan Piao."

ORIGIN
Query Match 2.7%; Score 26; DB 14; Length 444;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 545 CTTCCTCTTCTGAGCTCTCTGCAA 570
DB 388 CTTCCTCTTCTGAGCTCTCTGCAA 363

RESULT 10
CA860338/c 472 bp mRNA linear EST 20-DEC-2002

K0982C03-5N NIA Mouse Neural Stem Cell (Undifferentiated) cDNA Library (Long) Mus musculus cDNA clone NIA:K0982C03 IMAGE:30092090
5', mRNA sequence.
ACCESSION CA860338
VERSION CA860338.1 GI:27331887
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 472)
AUTHORS Piao, Y., Dudekula, D.B., Qian, Y., Martin, P.R., Alpa, K., Vescovi, A.L. and Ko, M.S.H.
TITLE Systematic Analyses of NIA Mouse Neural Stem Cell (Undifferentiated) cDNA Library (Long)
JOURNAL Unpublished (2002)
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: K0982 row: C column: 03
Seq primer: -21M13 Reverse
High quality sequence stop: 472
POLYA=No.

FEATURES
source
1. .472
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CD1"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="NIA:K0982C03 IMAGE:30092090"
/dev_stage="Adult"
/lab_host="DH108"
/lab_host="DH108"
/clone_lib="NIA Mouse Neural Stem Cell (Undifferentiated) cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Dr. Angelo L. Vescovi (Institute for Stem Cell Research, Italy). Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTCTAGATCGAGCGCGCCCTTTTCTTTT-3'] from 2.0 Microgram of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lona-linker LL-SalI, purified by phenol/chloroform, and separated from free linkers by centrifugation 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and centrifugation 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH108 E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.8 kb. The library was constructed by Yulan Piao."

ORIGIN
Query Match 2.7%; Score 26; DB 14; Length 472;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 545 CTTCCTCTTCTGAGCTCTCTGCAA 570
DB 388 CTTCCTCTTCTGAGCTCTCTGCAA 363

RESULT 11
B04945/c

LOCUS B04945 492 bp DNA linear GSS 13-JUL-1996
 DEFINITION CSRL-50F8-v CSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone CSRL-50F8, genomic survey sequence.
 ACCESSION B04945
 VERSION B04945.1 GI:1414223
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 492)
 Evans, G.A., Burbee, D., Davies, C., Hahner, L., Oliver, T., Gilbert, M., Jones, D., Ward, T., Gillilan, E., Schagemann, J., Probst, S., Harris, J., Depord, J., McFarland, J., Burzinski, K., Khan, M., Kuffer, K. and Garner, H.R.
 Genomic Sequence Sampled Map of Chromosome 11
 Unpublished (1996)
 CONTACT: Evans GA, Shane Probst
 McDermott Center for Human Growth and Development
 University of Texas Southwestern Medical Center At Dallas
 5323 Harry Hines Blvd, Dallas TX 75235-8591
 Tel: 214-648-1600
 Fax: 214-648-1666
 Email: gjevans@utsw.swmed.edu, shanemcdermott.swmed.edu
 PCR Primers
 FORWARD: GACTAGAGAGAGAAAATGCG
 BACKWARD: TTATCTCAATTGTGCTTC
 Seq primer: T7
 Class: cosmid ends
 High quality sequence stop: 492.
 Location/Qualifiers
 1..492
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="CSRL-50F8"
 /sex="female"
 /cell_type="chimeric hamster somatic cell hybrid"
 /clone_lib="CSRL flow sorted Chromosome 11 specific cosmid"
 /note="Vector: scos-1; Human Chromosome 11 specific cosmid library prepared from flow sorted human Chromosome 11 derived from Chinese Hamster Ovary (CHO) monochromosomal somatic cell hybrid, J1"

ORIGIN
 Query Match 2.7%; Score 26; DB 28; Length 492;
 Best Local Similarity 100.0%; Pred. No. 0.052;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 233 ATTCCCAAAATCGATGATGTTTGT 258
 |||||||
 137 ATTCCCAAAATCGATGATGTTTGT 112

RESULT 12
 BH418698/c 877 bp DNA linear GSS 12-DEC-2001
 LOCUS BH418698
 DEFINITION BOGT281TF BOGT Brassica oleracea genomic clone BOGT281, genomic survey sequence.
 ACCESSION BH418698
 VERSION BH418698.1 GI:17604426
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 877)
 Town, C.D., Van Aken, S., Uteback, T., Koo, H. and Fraser, C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished (2001)
 Other_GSSs: BOGT281TR

CONTACT: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.
 Location/Qualifiers
 1..877
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="TO.000DH3"
 /db_xref="taxon:3712"
 /clone="BOGT281"
 /note="Vector: PHOS1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"

ORIGIN
 Query Match 2.7%; Score 26; DB 28; Length 877;
 Best Local Similarity 100.0%; Pred. No. 0.053;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 307 CTCTCTCTGTTCTTTGTTCTTTCTG 332
 |||||||
 118 CTCTCTCTGTTCTTTGTTCTTTCTG 93

RESULT 13
 AY405611 903 bp DNA linear GSS 16-DEC-2003
 LOCUS AY405611
 DEFINITION Mus musculus OR888 gene, VIRUAL TRANSCRIPT, partial sequence, genomic survey sequence.
 ACCESSION AY405611
 VERSION AY405611.1 GI:39761585
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 903)
 Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriter, S., Wang, G., Zheng, X.H., White, T.D., Sninsky, J.J., Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 Science 302 (5652), 1960-1963 (2003)
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 2 (bases 1 to 903)
 Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriter, S., Wang, G., Zheng, X.H., White, T.D., Sninsky, J.J., Adams, M.D. and Cargill, M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering them based on alignment.
 Location/Qualifiers
 1..903
 /organism="Mus musculus"
 /mol_type="genomic DNA"
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 /gene="OR888"
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 TCTTCTCCGTTTCTAGGTTCTAC 106
 47 TCTTCTCTCTGTTTCTAGGTTCTAC 72

RESULT 14
 LOCUS AY407111 933 bp DNA linear GSS 15-DEC-2003
 DEFINITION Mus musculus OR6B12 gene, VIRITAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY407111
 VERSION AY407111.1 GI:39763082
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 933)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sniasky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene titers
 Science 302 (5652), 1960-1963 (2003)
 14671302
 2 (bases 1 to 933)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sniasky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submision
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

FEATURES
 Location/Qualifiers
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ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 0.053;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 545 CTTCCCTTCTTGTAGCTCTCTGCAA 570
 541 CTTCCCTTCTTGTAGCTCTCTGCAA 566

RESULT 15
 LOCUS CE158635 625 bp DNA linear GSS 25-SEP-2003
 DEFINITION tigr-gss-dog-17000371402682 Dog Library Canis familiaris genomic,
 genomic survey sequence.
 ACCESSION CE158635
 VERSION CE158635.1 GI:35286025
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 625)
 Kirkness,B.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
 Venter,J.C.

TITLE The dog genome: survey sequencing and comparative analysis
 JOURNAL Science 301 (5641), 1898-1903 (2003)
 MEDLINE 22875432
 PUBMED 14512627

COMMENT
 Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirkness@tigr.org
 Class: Shotgun.
 Location/Qualifiers
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 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN
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QY 81 TCTTCTCCGTTTCTAGGTTCTCA 105
 162 TCTTCTCCGTTTCTAGGTTCTCA 186

Search completed: September 30, 2004, 08:14:33
 Job time : 3092 secs

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